

SEQUENCE LISTING

<110> ISIS INNOVATION LIMITED

<120> HYDROGEN PEROXIDE OXIDATION

<130> N.91079A SA

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<170> PatentIn version 3.2

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tat att tgc gga gac gga agc caa atg gca cct gcc gtt gaa gca Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala Val Glu Ala 1000 1005 1010	4576
acg ctt atg aaa agc tat gct gac gtt cac caa gtg agt gaa gca	4621

Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser Glu Ala
 1015 1020 1025
 gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc cga tac 4666
 Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly Arg Tyr
 1030 1035 1040
 gca aaa gac gtg tgg gct ggg taa attaaaaaga ggctaggata aaagtagttt 4720
 Ala Lys Asp Val Trp Ala Gly
 1045
 agttggttga aggaagatcc gaacgatgaa tcgttcggat cttttttattg gtagagtaaa 4780
 cgtagatttc atctatttag tgacttgtag cggttgattg gagggcaagg tgaagactcc 4840
 aatcaaccgc ggtgtcacat gcaagccata cgaaattcat ttctcccatt tattcgtctt 4900
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 Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp
 50 55 60
 Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg
 65 70 75 80
 Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn
 85 90 95
 Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala
 100 105 110
 Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val
 115 120 125
 Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu
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 Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn
 145 150 155 160
 Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr
 165 170 175
 Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala
 180 185 190
 Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu
 195 200 205
 Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg
 210 215 220
 Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn
 225 230 235 240
 Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg
 245 250 255

Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly
 260 265 270
 Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu
 275 280 285
 Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro
 290 295 300
 Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn
 305 310 315 320
 Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala
 325 330 335
 Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp
 340 345 350
 Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp
 355 360 365
 Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser
 370 375 380
 Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala
 385 390 395 400
 Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly
 405 410 415
 Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu
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 Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys
 435 440 445
 Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr
 450 455 460
 Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn
 465 470 475 480
 Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly
 485 490 495
 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro
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 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly
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 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn
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 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala
 565 570 575
 Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala
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 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp
 595 600 605
 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp
 610 615 620
 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys
 625 630 635 640
 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu
 645 650 655
 Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu

660	665	670
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Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile		
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Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly		
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Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu		
725	730	735
Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln		
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Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met		
755	760	765
Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu		
770	775	780
Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr		
785	790	795
Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser		
805	810	815
Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile		
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Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser		
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Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile		
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Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu		
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Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg		
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Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu		
915	920	925
Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr		
930	935	940
Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr		
945	950	955
Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val		
965	970	975
Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp		
980	985	990
Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro		
995	1000	1005
Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln		
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Val Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu		
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Lys Gly Arg Tyr Ala Lys Asp Val Trp Ala Gly		
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 <223> Cytochrome P450BM-3 mutant

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 tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa att 96
 Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
 20 25 30
 gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt gta 144
 Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
 35 40 45
 acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat gaa 192
 Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
 50 55 60
 tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt gat 240
 Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
 65 70 75 80
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 Phe Ala Gly Asp Gly Leu Ala Thr Ser Trp Thr His Glu Lys Asn Trp
 85 90 95
 aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca atg 336
 Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
 100 105 110
 aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt caa 384
 Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
 115 120 125
 aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa gac 432
 Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
 130 135 140
 atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac tat 480
 Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
 145 150 155 160
 cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca agt 528
 Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
 165 170 175
 atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca aat 576
 Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
 180 185 190
 cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa gat 624
 Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
 195 200 205
 atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc aaa 672
 Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
 210 215 220
 gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac gga 720
 Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
 225 230 235 240
 aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc tat 768
 Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr

245	250	255	
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tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac gaa Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu 305 310 315 320			960
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gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac gaa Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu 340 345 350			1056
cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg gga Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly 355 360 365			1104
gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt gcg Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala 370 375 380			1152
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atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg gat Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp 420 425 430			1296
att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa gca Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala 435 440 445			1344
aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act gaa Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu 450 455 460			1392
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gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga gct Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala 515 520 525			1584
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aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta aaa Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys 545 550 555			1680

545	550	555	560	
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Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr	565	570	575	
acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct aaa				1776
Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys	580	585	590	
ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac gac				1824
Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp	595	600	605	
ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac gta				1872
Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val	610	615	620	
gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa tct				1920
Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser	625	630	635	640
act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt gcg				1968
Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala	645	650	655	
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Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu	660	665	670	
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Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu	675	680	685	
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Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro	690	695	700	
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Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu	705	710	715	720
gat gca tca cag caa atc cgt ctg gaa gca gaa gaa gaa aaa tta gct				2208
Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala	725	730	735	
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His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr	740	745	750	
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Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala	755	760	765	
gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg ctt				2352
Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu	770	775	780	
gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca atg				2400
Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met	785	790	795	800
ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc gaa				2448
Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu	805	810	815	
ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att tct				2496
Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser	820	825	830	
tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc gtt				2544
Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val	835	840	845	
gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att gcg				2592
Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala				

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Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
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att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa acg      2688
Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
885              890              895

ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga ggc      2736
Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
900              905              910

ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt gga      2784
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915              920              925

gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat ctg      2832
Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
930              935              940

tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg ctt      2880
Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
945              950              955              960

cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt cag      2928
His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
965              970              975

cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat caa      2976
His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
980              985              990

gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct gcc      3024
Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
995              1000              1005

gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg      3069
Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
1010              1015              1020

agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa      3114
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys
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<211> 1048

<212> PRT

<213> Artificial sequence

<220>

<223> Cytochrome P450BM-3 mutant

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20              25              30

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Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
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Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
50              55              60

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Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
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Phe Ala Gly Asp Gly Leu Ala Thr Ser Trp Thr His Glu Lys Asn Trp
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 Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
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 Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
 115 120 125
 Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
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 Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
 165 170 175
 Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
 180 185 190
 Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
 195 200 205
 Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
 210 215 220
 Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
 225 230 235 240
 Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr
 245 250 255
 Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu
 260 265 270
 Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln
 275 280 285
 Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser
 290 295 300
 Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu
 305 310 315 320
 Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys
 325 330 335
 Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu
 340 345 350
 Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly
 355 360 365
 Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala
 370 375 380
 Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys
 385 390 395 400
 Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met
 405 410 415
 Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp
 420 425 430
 Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala
 435 440 445
 Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu
 450 455 460
 Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr
 465 470 475 480
 Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr

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Val	Ala	Thr	Leu	Asp	Ser	His	Ala	Gly	Asn	Leu	Pro	Arg	Glu	Gly	Ala				
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Lys	Gln	Phe	Val	Asp	Trp	Leu	Asp	Gln	Ala	Ser	Ala	Asp	Glu	Val	Lys				
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Gly	Val	Arg	Tyr	Ser	Val	Phe	Gly	Cys	Gly	Asp	Lys	Asn	Trp	Ala	Thr				
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Thr	Tyr	Gln	Lys	Val	Pro	Ala	Phe	Ile	Asp	Glu	Thr	Leu	Ala	Ala	Lys				
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Gly	Ala	Glu	Asn	Ile	Ala	Asp	Arg	Gly	Glu	Ala	Asp	Ala	Ser	Asp	Asp				
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Phe	Glu	Gly	Thr	Tyr	Glu	Glu	Trp	Arg	Glu	His	Met	Trp	Ser	Asp	Val				
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Ala	Ala	Tyr	Phe	Asn	Leu	Asp	Ile	Glu	Asn	Ser	Glu	Asp	Asn	Lys	Ser				
625					630					635				640					
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705              710              715              720
Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala
              725              730              735
His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr
              740              745              750
Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala
              755              760              765
Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu
              770              775              780
Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met
785              790              795              800
Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu
              805              810              815
Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser
              820              825              830
Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val
              835              840              845
Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala
              850              855              860
Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe
865              870              875              880
Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr
              885              890              895
Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly
              900              905              910
Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly
              915              920              925
Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu
              930              935              940
Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu
945              950              955              960
His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln
              965              970              975
His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln
              980              985              990
Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala
              995              1000              1005
Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val
              1010              1015              1020
Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys
              1025              1030              1035
Gly Arg Tyr Ala Lys Asp Val Trp Ala Gly
              1040              1045

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<210> 9
<211> 1032
<212> DNA
<213> Nocardia corallina

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<220>
<221> CDS
<222> (1)..(1032)

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<400> 9
atg acg aca gag gcg acg gtg gcc cga ccg gtg gag ctc gaa ggt cac      48
Met Thr Thr Glu Ala Thr Val Ala Arg Pro Val Glu Leu Glu Gly His
1      5      10      15

cgg aca ttc acc tgg ttc acg ccc gcc agg cga aag ccg acg gag tac      96
Arg Thr Phe Thr Trp Phe Thr Pro Ala Arg Arg Lys Pro Thr Glu Tyr
20      25      30

gag ctc tac acc gtg ggt caa cag tcc act ccg gac gag tgg ctg cat      144
Glu Leu Tyr Thr Val Gly Gln Gln Ser Thr Pro Asp Glu Trp Leu His
35      40      45

gtg gac tgg ccg ctg cgc ttc gac gac ggc cgc gcc ccg tgg gag gag      192
Val Asp Trp Pro Leu Arg Phe Asp Asp Gly Arg Ala Pro Trp Glu Glu
50      55      60

gag tcg agt gcg gta cgg acc tcg gag tgg tcg gct tac cgc gac cca      240
Glu Ser Ser Ala Val Arg Thr Ser Glu Trp Ser Ala Tyr Arg Asp Pro
65      70      75      80

cac caa ctg tgg cag cgt ccc tac gtc agc acg tgc aac cag gac cag      288
His Gln Leu Trp Gln Arg Pro Tyr Val Ser Thr Cys Asn Gln Asp Gln
85      90      95

cag gcc ctc gcg cgg ctg gtc ccc gtc ctg acc atg ggg tcg gcg gcg      336
Gln Ala Leu Ala Arg Leu Val Pro Val Leu Thr Met Gly Ser Ala Ala
100      105      110

atc acg ccc atc tgg tcg cag aag atc ctc gcc agg tcc tac gcc gcc      384
Ile Thr Pro Ile Trp Ser Gln Lys Ile Leu Ala Arg Ser Tyr Ala Ala
115      120      125

tgg cca ttc gtc gag tac ggg ctc ttc ctg agc ctg gcc tac gcc gtg      432
Trp Pro Phe Val Glu Tyr Gly Leu Phe Leu Ser Leu Ala Tyr Ala Val
130      135      140

cgc cag gcc atg tcc gac acg gtc cag ttc agc gtg gtg ttc cag gcc      480
Arg Gln Ala Met Ser Asp Thr Val Gln Phe Ser Val Val Phe Gln Ala
145      150      155      160

gtg gac cgc atg cgg ctg ctc cag gac atc gtc cac cac ctg gac cac      528
Val Asp Arg Met Arg Leu Leu Gln Asp Ile Val His His Leu Asp His
165      170      175

ctg cag gag tcg ccg gaa ttc agc gac gcc ggg gcc cgc gag gcc tgg      576
Leu Gln Glu Ser Pro Glu Phe Ser Asp Ala Gly Ala Arg Glu Ala Trp
180      185      190

atg tcc gac tcc acc ctg gtc ccg atc cgg gaa gtg atc gag cgc atc      624
Met Ser Asp Ser Thr Leu Val Pro Ile Arg Glu Val Ile Glu Arg Ile
195      200      205

gcc gcc agc cag gac tgg gtg gag atc ctg gtc gcc ggc acg ctc gtc      672
Ala Ala Ser Gln Asp Trp Val Glu Ile Leu Val Ala Gly Thr Leu Val
210      215      220

ttc gag cct ctg gtc ggc cac ctg gcg aag gcc gag ttg ttc agc cgc      720
Phe Glu Pro Leu Val Gly His Leu Ala Lys Ala Glu Leu Phe Ser Arg
225      230      235      240

cgt gcg cca atg ttc ggg gac ggg acc acg ccg gcg gtg ctg gcg tcg      768
Arg Ala Pro Met Phe Gly Asp Gly Thr Thr Pro Ala Val Leu Ala Ser
245      250      255

gcc ctg ctg gac agc ggc agg cac ctc gaa tcg gtc cag gcg ctc gtc      816
Ala Leu Leu Asp Ser Gly Arg His Leu Glu Ser Val Gln Ala Leu Val
260      265      270

cgc ctc gtc tgc caa gac ccc gtc cat ggc gac cag aac cag gcg act      864
Arg Leu Val Cys Gln Asp Pro Val His Gly Asp Gln Asn Gln Ala Thr
275      280      285

gtg cgg cgg tgg atc gag gaa tgg cag ccg cgg tgc aag gcg gcg gcc      912
Val Arg Arg Trp Ile Glu Glu Trp Gln Pro Arg Cys Lys Ala Ala Ala
290      295      300

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cag tcc ttc ctg ccg acg ttc tcc gac tgc ggc atc gac gcc aag gaa 960
 Gln Ser Phe Leu Pro Thr Phe Ser Asp Cys Gly Ile Asp Ala Lys Glu
 305 310 315 320

agc gcc aac gcg ctg tcc cgg gcg ctg gcg aac cag cgg gcc gcc gtc 1008
 Ser Ala Asn Ala Leu Ser Arg Ala Leu Ala Asn Gln Arg Ala Ala Val
 325 330 335

gag ggc gcc ggc atc acg gca tga 1032
 Glu Gly Ala Gly Ile Thr Ala
 340

<210> 10
 <211> 343
 <212> PRT
 <213> *Nocardia corallina*

<400> 10

Met Thr Thr Glu Ala Thr Val Ala Arg Pro Val Glu Leu Glu Gly His
 1 5 10 15

Arg Thr Phe Thr Trp Phe Thr Pro Ala Arg Arg Lys Pro Thr Glu Tyr
 20 25 30

Glu Leu Tyr Thr Val Gly Gln Gln Ser Thr Pro Asp Glu Trp Leu His
 35 40 45

Val Asp Trp Pro Leu Arg Phe Asp Asp Gly Arg Ala Pro Trp Glu Glu
 50 55 60

Glu Ser Ser Ala Val Arg Thr Ser Glu Trp Ser Ala Tyr Arg Asp Pro
 65 70 75 80

His Gln Leu Trp Gln Arg Pro Tyr Val Ser Thr Cys Asn Gln Asp Gln
 85 90 95

Gln Ala Leu Ala Arg Leu Val Pro Val Leu Thr Met Gly Ser Ala Ala
 100 105 110

Ile Thr Pro Ile Trp Ser Gln Lys Ile Leu Ala Arg Ser Tyr Ala Ala
 115 120 125

Trp Pro Phe Val Glu Tyr Gly Leu Phe Leu Ser Leu Ala Tyr Ala Val
 130 135 140

Arg Gln Ala Met Ser Asp Thr Val Gln Phe Ser Val Val Phe Gln Ala
 145 150 155 160

Val Asp Arg Met Arg Leu Leu Gln Asp Ile Val His His Leu Asp His
 165 170 175

Leu Gln Glu Ser Pro Glu Phe Ser Asp Ala Gly Ala Arg Glu Ala Trp
 180 185 190

Met Ser Asp Ser Thr Leu Val Pro Ile Arg Glu Val Ile Glu Arg Ile
 195 200 205

Ala Ala Ser Gln Asp Trp Val Glu Ile Leu Val Ala Gly Thr Leu Val
 210 215 220

Phe Glu Pro Leu Val Gly His Leu Ala Lys Ala Glu Leu Phe Ser Arg
 225 230 235 240

Arg Ala Pro Met Phe Gly Asp Gly Thr Thr Pro Ala Val Leu Ala Ser
 245 250 255

Ala Leu Leu Asp Ser Gly Arg His Leu Glu Ser Val Gln Ala Leu Val
 260 265 270

Arg Leu Val Cys Gln Asp Pro Val His Gly Asp Gln Asn Gln Ala Thr
 275 280 285

Val Arg Arg Trp Ile Glu Glu Trp Gln Pro Arg Cys Lys Ala Ala Ala

26

290	295	300	
Gln Ser Phe Leu Pro Thr Phe Ser Asp Cys Gly Ile Asp Ala Lys Glu			
305	310	315	320
Ser Ala Asn Ala Leu Ser Arg Ala Leu Ala Asn Gln Arg Ala Ala Val			
	325	330	335
Glu Gly Ala Gly Ile Thr Ala			
	340		
<210> 11			
<211> 1506			
<212> DNA			
<213> Nocardia corallina			
<220>			
<221> CDS			
<222> (1)..(1506)			
<400> 11			
atg gca tcg aac ccc acc cag ctc cac gag aag tcg aag tcc tac gac			48
Met Ala Ser Asn Pro Thr Gln Leu His Glu Lys Ser Lys Ser Tyr Asp			
1	5	10	15
tgg gac ttc acc tcc gtc gag cgg cgc ccc aag ttc gag acg aag tac			96
Trp Asp Phe Thr Ser Val Glu Arg Arg Pro Lys Phe Glu Thr Lys Tyr			
	20	25	30
aag atg ccc aag aag ggc aag gac ccg ttc cgc gtc ctg atc cgt gac			144
Lys Met Pro Lys Lys Gly Lys Asp Pro Phe Arg Val Leu Ile Arg Asp			
	35	40	45
tac atg aag atg gaa gcg gag aag gac gac cgg acc cat ggc ttc ctc			192
Tyr Met Lys Met Glu Ala Glu Lys Asp Asp Arg Thr His Gly Phe Leu			
	50	55	60
gac ggc gcc gtg cgg acg cgt gag gcc acc agg att gag ccg cgg ttc			240
Asp Gly Ala Val Arg Thr Arg Glu Ala Thr Arg Ile Glu Pro Arg Phe			
65	70	75	80
gct gag gcc atg aag atc atg gtg ccg cag ctg acc aac gcc gag tac			288
Ala Glu Ala Met Lys Ile Met Val Pro Gln Leu Thr Asn Ala Glu Tyr			
	85	90	95
cag gcg gtg gcg ggc tgc gga atg atc atc tcg gcc gtc gag aac cag			336
Gln Ala Val Ala Gly Cys Gly Met Ile Ile Ser Ala Val Glu Asn Gln			
	100	105	110
gag ctc cgt cag ggc tac gcc gct cag atg ctc gat gag gtg cgg cac			384
Glu Leu Arg Gln Gly Tyr Ala Ala Gln Met Leu Asp Glu Val Arg His			
	115	120	125
gcg cag ctc gag atg acg cta cgc aac tac tac gcg aag cac tgg tgc			432
Ala Gln Leu Glu Met Thr Leu Arg Asn Tyr Tyr Ala Lys His Trp Cys			
	130	135	140
gat ccc tcc ggc ttc gac atc ggt cag cgc ggc ctg tac cag cac ccc			480
Asp Pro Ser Gly Phe Asp Ile Gly Gln Arg Gly Leu Tyr Gln His Pro			
145	150	155	160
gcg ggg ctg gtg tcc atc ggc gag ttc cag cac ttc aat act ggt gac			528
Ala Gly Leu Val Ser Ile Gly Glu Phe Gln His Phe Asn Thr Gly Asp			
	165	170	175
ccg ctt gac gtc atc atc gat ctc aac atc gtg gcc gag acg gcg ttc			576
Pro Leu Asp Val Ile Ile Asp Leu Asn Ile Val Ala Glu Thr Ala Phe			
	180	185	190
acg aac atc ctg ctg gtg gcc act cca cag gtc gcc gtg gcc aac ggg			624
Thr Asn Ile Leu Leu Val Ala Thr Pro Gln Val Ala Val Ala Asn Gly			
	195	200	205
gac aac gcg atg gcc agc gtg ttc ctc tcg atc cag tcg gac gag gcc			672

Asp Asn Ala Met Ala Ser Val Phe Leu Ser Ile Gln Ser Asp Glu Ala 210 215 220	
agg cac atg gcc aac ggg tac ggc tcg gtc atg gcg ctg ctg gag aac Arg His Met Ala Asn Gly Tyr Gly Ser Val Met Ala Leu Leu Glu Asn 225 230 235 240	720
gag gac aac ctc ccg ctg ctc aac cag tct ctc gat cgg cac ttc tgg Glu Asp Asn Leu Pro Leu Leu Asn Gln Ser Leu Asp Arg His Phe Trp 245 250 255	768
cgt gcc cac aag gcc ttg gac aac gcg gtc gga tgg tgt tcg gag tat Arg Ala His Lys Ala Leu Asp Asn Ala Val Gly Trp Cys Ser Glu Tyr 260 265 270	816
ggc gcc cgc aag cgg cca tgg agc tac aag gcc cag tgg gag gaa tgg Gly Ala Arg Lys Arg Pro Trp Ser Tyr Lys Ala Gln Trp Glu Glu Trp 275 280 285	864
gtc gtc gac gac ttc gtg ggc ggc tac atc gac cga ctc agc gag ttc Val Val Asp Asp Phe Val Gly Gly Tyr Ile Asp Arg Leu Ser Glu Phe 290 295 300	912
ggc gtt cag gct ccg gcc tgc ctt ggc gcg gcc gcc gac gag gtc aag Gly Val Gln Ala Pro Ala Cys Leu Gly Ala Ala Ala Asp Glu Val Lys 305 310 315 320	960
tgg tcg cac cac acg ctc ggt cag gtg ctg tcg gcg gtg tgg ccg ctg Trp Ser His His Thr Leu Gly Gln Val Leu Ser Ala Val Trp Pro Leu 325 330 335	1008
aac ttc tgg cgc tcg gac gcc atg gga ccg gcg gac ttc gag tgg ttc Asn Phe Trp Arg Ser Asp Ala Met Gly Pro Ala Asp Phe Glu Trp Phe 340 345 350	1056
gag aac cac tac ccg ggc tgg agc gcg gcc tac cag ggt tac tgg gag Glu Asn His Tyr Pro Gly Trp Ser Ala Ala Tyr Gln Gly Tyr Trp Glu 355 360 365	1104
ggc tac aag gcg ctc gcc gac cca gca ggc gga cgc atc atg ctc cag Gly Tyr Lys Ala Leu Ala Asp Pro Ala Gly Gly Arg Ile Met Leu Gln 370 375 380	1152
gag ctg ccg ggt ctg ccg ccg atg tgt cag gtg tgc cag gtg ccg tgc Glu Leu Pro Gly Leu Pro Pro Met Cys Gln Val Cys Gln Val Pro Cys 385 390 395 400	1200
gtg atg ccg cgg ctg gat atg aac gcc gcg cgg atc atc gag ttc gag Val Met Pro Arg Leu Asp Met Asn Ala Ala Arg Ile Ile Glu Phe Glu 405 410 415	1248
ggg cag aaa atc gcg ctg tgc agc gaa ccc tgc cag cgg atc ttc acc Gly Gln Lys Ile Ala Leu Cys Ser Glu Pro Cys Gln Arg Ile Phe Thr 420 425 430	1296
aac tgg ccg gag gcg tac cgc cac cgc aag caa tac tgg gcc cgc tac Asn Trp Pro Glu Ala Tyr Arg His Arg Lys Gln Tyr Trp Ala Arg Tyr 435 440 445	1344
cac gga tgg gac ctg gcg gac gtc atc gtt gat ctc ggc tac atc cgc His Gly Trp Asp Leu Ala Asp Val Ile Val Asp Leu Gly Tyr Ile Arg 450 455 460	1392
ccg gac ggc aag acc ctc atc ggc cag ccg ctg ctc gag atg gag cgg Pro Asp Gly Lys Thr Leu Ile Gly Gln Pro Leu Leu Glu Met Glu Arg 465 470 475 480	1440
ctg tgg acc atc gac gac atc cgg gcc ctt cag tac gaa gtc aag gac Leu Trp Thr Ile Asp Asp Ile Arg Ala Leu Gln Tyr Glu Val Lys Asp 485 490 495	1488
ccg ttg cag gag gcg tga Pro Leu Gln Glu Ala 500	1506

<210> 12
 <211> 501
 <212> PRT
 <213> Nocardia corallina

<400> 12

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Met Ala Ser Asn Pro Thr Gln Leu His Glu Lys Ser Lys Ser Tyr Asp
1          5          10          15

Trp Asp Phe Thr Ser Val Glu Arg Arg Pro Lys Phe Glu Thr Lys Tyr
          20          25          30

Lys Met Pro Lys Lys Gly Lys Asp Pro Phe Arg Val Leu Ile Arg Asp
          35          40          45

Tyr Met Lys Met Glu Ala Glu Lys Asp Asp Arg Thr His Gly Phe Leu
50          55          60

Asp Gly Ala Val Arg Thr Arg Glu Ala Thr Arg Ile Glu Pro Arg Phe
65          70          75          80

Ala Glu Ala Met Lys Ile Met Val Pro Gln Leu Thr Asn Ala Glu Tyr
          85          90          95

Gln Ala Val Ala Gly Cys Gly Met Ile Ile Ser Ala Val Glu Asn Gln
          100          105          110

Glu Leu Arg Gln Gly Tyr Ala Ala Gln Met Leu Asp Glu Val Arg His
          115          120          125

Ala Gln Leu Glu Met Thr Leu Arg Asn Tyr Tyr Ala Lys His Trp Cys
          130          135          140

Asp Pro Ser Gly Phe Asp Ile Gly Gln Arg Gly Leu Tyr Gln His Pro
          145          150          155          160

Ala Gly Leu Val Ser Ile Gly Glu Phe Gln His Phe Asn Thr Gly Asp
          165          170          175

Pro Leu Asp Val Ile Ile Asp Leu Asn Ile Val Ala Glu Thr Ala Phe
          180          185          190

Thr Asn Ile Leu Leu Val Ala Thr Pro Gln Val Ala Val Ala Asn Gly
          195          200          205

Asp Asn Ala Met Ala Ser Val Phe Leu Ser Ile Gln Ser Asp Glu Ala
          210          215          220

Arg His Met Ala Asn Gly Tyr Gly Ser Val Met Ala Leu Leu Glu Asn
          225          230          235          240

Glu Asp Asn Leu Pro Leu Leu Asn Gln Ser Leu Asp Arg His Phe Trp
          245          250          255

Arg Ala His Lys Ala Leu Asp Asn Ala Val Gly Trp Cys Ser Glu Tyr
          260          265          270

Gly Ala Arg Lys Arg Pro Trp Ser Tyr Lys Ala Gln Trp Glu Glu Trp
          275          280          285

Val Val Asp Asp Phe Val Gly Gly Tyr Ile Asp Arg Leu Ser Glu Phe
          290          295          300

Gly Val Gln Ala Pro Ala Cys Leu Gly Ala Ala Ala Asp Glu Val Lys
          305          310          315          320

Trp Ser His His Thr Leu Gly Gln Val Leu Ser Ala Val Trp Pro Leu
          325          330          335

Asn Phe Trp Arg Ser Asp Ala Met Gly Pro Ala Asp Phe Glu Trp Phe
          340          345          350

Glu Asn His Tyr Pro Gly Trp Ser Ala Ala Tyr Gln Gly Tyr Trp Glu
          355          360          365

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Gly Tyr Lys Ala Leu Ala Asp Pro Ala Gly Gly Arg Ile Met Leu Gln
370 375 380

Glu Leu Pro Gly Leu Pro Pro Met Cys Gln Val Cys Gln Val Pro Cys
385 390 395 400

Val Met Pro Arg Leu Asp Met Asn Ala Ala Arg Ile Ile Glu Phe Glu
405 410 415

Gly Gln Lys Ile Ala Leu Cys Ser Glu Pro Cys Gln Arg Ile Phe Thr
420 425 430

Asn Trp Pro Glu Ala Tyr Arg His Arg Lys Gln Tyr Trp Ala Arg Tyr
435 440 445

His Gly Trp Asp Leu Ala Asp Val Ile Val Asp Leu Gly Tyr Ile Arg
450 455 460

Pro Asp Gly Lys Thr Leu Ile Gly Gln Pro Leu Leu Glu Met Glu Arg
465 470 475 480

Leu Trp Thr Ile Asp Asp Ile Arg Ala Leu Gln Tyr Glu Val Lys Asp
485 490 495

Pro Leu Gln Glu Ala
500

<210> 13
<211> 1494
<212> DNA
<213> Xanthobacta sp.

<220>
<221> CDS
<222> (1)..(1494)

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Met Ala Leu Leu Asn Arg Asp Asp Trp Tyr Asp Ile Ala Arg Asp Val
1 5 10 15
gac tgg acg ctc agc tat gtc gac cgc gcg gtc gcc ttt ccc gag gag 96
Asp Trp Thr Leu Ser Tyr Val Asp Arg Ala Val Ala Phe Pro Glu Glu
20 25 30
tgg aaa ggc gaa aag gac att tgc ggc acg gcc tgg gac gat tgg gac 144
Trp Lys Gly Glu Lys Asp Ile Cys Gly Thr Ala Trp Asp Asp Trp Asp
35 40 45
gag ccc ttc cgg gtc tcc ttc cgc gaa tat gtg atg gtc cag cgc gac 192
Glu Pro Phe Arg Val Ser Phe Arg Glu Tyr Val Met Val Gln Arg Asp
50 55 60
aag gaa gcg agc gtc ggc gcc atc cgc gag gcc atg gtc cgc gcc aag 240
Lys Glu Ala Ser Val Gly Ala Ile Arg Glu Ala Met Val Arg Ala Lys
65 70 75 80
gcc tat gag aag ctc gac gac ggc cac aag gcc acc tcg cac ctg cac 288
Ala Tyr Glu Lys Leu Asp Asp Gly His Lys Ala Thr Ser His Leu His
85 90 95
atg ggc acc atc acc atg gtg gag cac atg gcg gtc acc atg cag agc 336
Met Gly Thr Ile Thr Met Val Glu His Met Ala Val Thr Met Gln Ser
100 105 110
cgg ttc gtg cgc ttc gcg ccg tcc gcc cgc tgg cgc agc ctc ggg gcg 384
Arg Phe Val Arg Phe Ala Pro Ser Ala Arg Trp Arg Ser Leu Gly Ala
115 120 125
ttc ggc atg ctg gac gag acc cgc cac acc cag ctg gac ctg cgc ttc 432
Phe Gly Met Leu Asp Glu Thr Arg His Thr Gln Leu Asp Leu Arg Phe
130 135 140
agc cac gat ctg ctc aac gat tcc ccg agc ttc gac tgg agc cag cgg 480

Ser 145	His	Asp	Leu	Leu	Asn 150	Asp	Ser	Pro	Ser	Phe 155	Asp	Trp	Ser	Gln	Arg 160	
gcg	ttc	cac	acc	gac	gaa	tgg	gcg	gtt	ctc	gcc	acc	cgc	aac	ctg	ttc	528
Ala	Phe	His	Thr	Asp 165	Glu	Trp	Ala	Val 170	Leu	Ala	Thr	Arg	Asn	Leu 175	Phe	
gac	gac	atc	atg	ctc	aac	gcc	gac	tgc	gtg	gag	gcg	gcg	ctc	gcc	acc	576
Asp	Asp	Ile	Met 180	Leu	Asn	Ala	Asp	Cys 185	Val	Glu	Ala	Ala	Leu 190	Ala	Thr	
agc	ctg	acg	ctg	gag	cac	ggc	ttc	acc	aac	atc	cag	ttc	gtg	gcg	ctc	624
Ser	Leu	Thr 195	Leu	Glu	His	Gly	Phe 200	Thr	Asn	Ile	Gln	Phe 205	Val	Ala	Leu	
gcc	tcc	gac	gcc	atg	gaa	gcc	ggc	gac	gtg	aac	ttc	tcc	aac	ctc	ttg	672
Ala	Ser 210	Asp	Ala	Met	Glu	Ala 215	Gly	Asp	Val	Asn	Phe 220	Ser	Asn	Leu	Leu	
tcg	agc	atc	cag	acc	gac	gag	gcg	cgg	cac	gcc	cag	ttg	ggc	ttt	ccc	720
Ser 225	Ser	Ile	Gln	Thr	Asp 230	Glu	Ala	Arg	His	Ala 235	Gln	Leu	Gly	Phe 240	Pro	
acc	ctc	gac	gtg	atg	atg	aag	cac	gac	ccc	aag	cgc	gcc	cag	cag	atc	768
Thr	Leu	Asp	Val 245	Met	Met	Lys	His	Asp 250	Pro	Lys	Arg	Ala	Gln	Gln 255	Ile	
ctg	gac	gtc	gcc	ttc	tgg	cgc	tcc	tac	cgc	atc	ttc	cag	gcg	gtg	acc	816
Leu	Asp	Val 260	Ala	Phe	Trp	Arg	Ser	Tyr 265	Arg	Ile	Phe	Gln 270	Ala	Val	Thr	
ggc	gtc	tcc	atg	gac	tac	tac	acg	ccg	gtc	gcc	aag	cgg	cag	atg	tcg	864
Gly	Val 275	Ser	Met	Asp	Tyr	Tyr	Thr 280	Pro	Val	Ala	Lys	Arg 285	Gln	Met	Ser	
ttc	aag	gag	ttc	atg	ctg	gag	tgg	atc	gtc	aag	cat	cat	gag	cgc	atc	912
Phe	Lys 290	Glu	Phe	Met	Leu	Glu 295	Trp	Ile	Val	Lys	His 300	His	Glu	Arg	Ile	
ctg	cgc	gac	tac	ggc	ctc	cag	aag	ccc	tgg	tac	tgg	gac	acg	ttc	gag	960
Leu 305	Arg	Asp	Tyr	Gly	Leu 310	Gln	Lys	Pro	Trp	Tyr 315	Trp	Asp	Thr	Phe 320	Glu	
aag	acc	ctc	gat	cac	ggc	cac	cac	gcg	ctg	cac	atc	ggc	acc	tgg	ttc	1008
Lys	Thr	Leu	Asp 325	His	Gly	His	His	Ala 330	Leu	His	Ile	Gly	Thr	Trp 335	Phe	
tgg	cgc	ccg	acc	ctg	ttc	tgg	gat	ccc	aat	ggc	ggc	gtc	tcg	cgc	gag	1056
Trp	Arg	Pro 340	Thr	Leu	Phe	Trp	Asp	Pro 345	Asn	Gly	Gly	Val 350	Ser	Arg	Glu	
gag	cgg	cgc	tgg	ctg	aac	cag	aag	tat	ccg	aac	tgg	gaa	gag	agc	tgg	1104
Glu	Arg 355	Arg	Trp	Leu	Asn	Gln	Lys 360	Tyr	Pro	Asn	Trp	Glu 365	Glu	Ser	Trp	
ggc	gtc	ctg	tgg	gac	gag	atc	atc	tcc	aac	atc	aat	gcg	ggc	aac	att	1152
Gly 370	Val	Leu	Trp	Asp	Glu	Ile 375	Ile	Ser	Asn	Ile	Asn 380	Ala	Gly	Asn	Ile	
gaa	aag	acc	ttg	ccc	gag	acg	ctg	ccg	atg	ctg	tgc	aac	gtc	acc	aac	1200
Glu 385	Lys	Thr	Leu	Pro 390	Glu	Thr	Leu	Pro	Met	Leu 395	Cys	Asn	Val	Thr 400	Asn	
ctg	ccc	atc	ggc	tcg	cac	tgg	gac	cgc	ttc	cac	ctg	aag	ccc	gag	cag	1248
Leu	Pro	Ile	Gly 405	Ser	His	Trp	Asp	Arg	Phe 410	His	Leu	Lys	Pro	Glu 415	Gln	
ctc	gtc	tac	aag	ggg	cgg	ctc	tac	acc	ttc	gac	agc	g				

Val Asp Arg Phe Ile Gly Gly Gln Ile Gln Pro Met Thr Ile Glu Gly
 450 455 460

gtg ctc aac tgg atg ggc ctg acg ccc gaa gtc atg ggc aag gac gtg 1440
 Val Leu Asn Trp Met Gly Leu Thr Pro Glu Val Met Gly Lys Asp Val
 465 470 475 480

ttc aac tac cgt tgg gcc ggc gat tac gcc gag aac cgg atc gcc gcc 1488
 Phe Asn Tyr Arg Trp Ala Gly Asp Tyr Ala Glu Asn Arg Ile Ala Ala
 485 490 495

gag taa 1494
 Glu

<210> 14
 <211> 497
 <212> PRT
 <213> Xanthobacta sp.

<400> 14

Met Ala Leu Leu Asn Arg Asp Asp Trp Tyr Asp Ile Ala Arg Asp Val
 1 5 10 15

Asp Trp Thr Leu Ser Tyr Val Asp Arg Ala Val Ala Phe Pro Glu Glu
 20 25 30

Trp Lys Gly Glu Lys Asp Ile Cys Gly Thr Ala Trp Asp Asp Trp Asp
 35 40 45

Glu Pro Phe Arg Val Ser Phe Arg Glu Tyr Val Met Val Gln Arg Asp
 50 55 60

Lys Glu Ala Ser Val Gly Ala Ile Arg Glu Ala Met Val Arg Ala Lys
 65 70 75 80

Ala Tyr Glu Lys Leu Asp Asp Gly His Lys Ala Thr Ser His Leu His
 85 90 95

Met Gly Thr Ile Thr Met Val Glu His Met Ala Val Thr Met Gln Ser
 100 105 110

Arg Phe Val Arg Phe Ala Pro Ser Ala Arg Trp Arg Ser Leu Gly Ala
 115 120 125

Phe Gly Met Leu Asp Glu Thr Arg His Thr Gln Leu Asp Leu Arg Phe
 130 135 140

Ser His Asp Leu Leu Asn Asp Ser Pro Ser Phe Asp Trp Ser Gln Arg
 145 150 155 160

Ala Phe His Thr Asp Glu Trp Ala Val Leu Ala Thr Arg Asn Leu Phe
 165 170 175

Asp Asp Ile Met Leu Asn Ala Asp Cys Val Glu Ala Ala Leu Ala Thr
 180 185 190

Ser Leu Thr Leu Glu His Gly Phe Thr Asn Ile Gln Phe Val Ala Leu
 195 200 205

Ala Ser Asp Ala Met Glu Ala Gly Asp Val Asn Phe Ser Asn Leu Leu 210
 215 220

Ser Ser Ile Gln Thr Asp Glu Ala Arg His Ala Gln Leu Gly Phe Pro
 225 230 235 240

Thr Leu Asp Val Met Met Lys His Asp Pro Lys Arg Ala Gln Gln Ile
 245 250 255

Leu Asp Val Ala Phe Trp Arg Ser Tyr Arg Ile Phe Gln Ala Val Thr
 260 265 270

Gly Val Ser Met Asp Tyr Tyr Thr Pro Val Ala Lys Arg Gln Met Ser
 275 280 285

Phe Lys Glu Phe Met Leu Glu Trp Ile Val Lys His His Glu Arg Ile
 290 295 300
 Leu Arg Asp Tyr Gly Leu Gln Lys Pro Trp Tyr Trp Asp Thr Phe Glu
 305 310 315 320
 Lys Thr Leu Asp His Gly His His Ala Leu His Ile Gly Thr Trp Phe
 325 330 335
 Trp Arg Pro Thr Leu Phe Trp Asp Pro Asn Gly Gly Val Ser Arg Glu
 340 345 350
 Glu Arg Arg Trp Leu Asn Gln Lys Tyr Pro Asn Trp Glu Glu Ser Trp
 355 360 365
 Gly Val Leu Trp Asp Glu Ile Ile Ser Asn Ile Asn Ala Gly Asn Ile
 370 375 380
 Glu Lys Thr Leu Pro Glu Thr Leu Pro Met Leu Cys Asn Val Thr Asn
 385 390 395 400
 Leu Pro Ile Gly Ser His Trp Asp Arg Phe His Leu Lys Pro Glu Gln
 405 410 415
 Leu Val Tyr Lys Gly Arg Leu Tyr Thr Phe Asp Ser Asp Val Ser Lys
 420 425 430
 Trp Ile Phe Glu Leu Asp Pro Glu Arg Tyr Ala Gly His Thr Asn Val
 435 440 445
 Val Asp Arg Phe Ile Gly Gly Gln Ile Gln Pro Met Thr Ile Glu Gly
 450 455 460
 Val Leu Asn Trp Met Gly Leu Thr Pro Glu Val Met Gly Lys Asp Val
 465 470 475 480
 Phe Asn Tyr Arg Trp Ala Gly Asp Tyr Ala Glu Asn Arg Ile Ala Ala
 485 490 495

Glu

<210> 15
 <211> 1026
 <212> DNA
 <213> Xanthobacta sp.

<220>
 <221> CDS
 <222> (1)..(1026)

<400> 15
 atg aca cag cag cgc ccc acc cgc acg cgc gag cgc aag aag acc tgg 48
 Met Thr Gln Gln Arg Pro Thr Arg Thr Arg Glu Arg Lys Lys Thr Trp
 1 5 10 15
 acg gct ttc ggc aat ctc gga cgc aag ccg acc gac tac gag gtc gtc 96
 Thr Ala Phe Gly Asn Leu Gly Arg Lys Pro Thr Asp Tyr Glu Val Val
 20 25 30
 acc cac aac atg aac cac acc atg cgc ggc acg ccc ctg gag ctg tcg 144
 Thr His Asn Met Asn His Thr Met Arg Gly Thr Pro Leu Glu Leu Ser
 35 40 45
 ccg acg gtg cac gcc aat gtg tgg ctc aag aag aac cgc gac gag atc 192
 Pro Thr Val His Ala Asn Val Trp Leu Lys Lys Asn Arg Asp Glu Ile
 50 55 60
 gcg ctc aag gtc gac agc tgg gat ctg ttc cgc gat ccc gac cgc acc 240
 Ala Leu Lys Val Asp Ser Trp Asp Leu Phe Arg Asp Pro Asp Arg Thr
 65 70 75 80
 acc tac gac acc tac gtc aag atg cag gac gac cag gag acc tat gtc 288

Thr	Tyr	Asp	Thr	Tyr	Val	Lys	Met	Gln	Asp	Asp	Gln	Glu	Thr	Tyr	Val		
				85					90					95			
gac aac ctg ctc ctg tcc tac acc ggc gag ggc cgc tac gac gag gag 336																	
Asp	Asn	Leu	Leu	Leu	Ser	Tyr	Thr	Gly	Glu	Gly	Arg	Tyr	Asp	Glu	Glu		
			100					105					110				
ctt tcc tcg cgc agc ctc gac ctc ctg tcc gcg ggg ctg acg ccg acc 384																	
Leu	Ser	Ser	Arg	Ser	Leu	Asp	Leu	Leu	Ser	Ala	Gly	Leu	Thr	Pro	Thr		
			115				120					125					
cgc tat ctg ggc cat ggg ctg cag atg ctc gcg gcc tat atc cag cag 432																	
Arg	Tyr	Leu	Gly	His	Gly	Leu	Gln	Met	Leu	Ala	Ala	Tyr	Ile	Gln	Gln		
		130				135					140						
ctc gcc ccg tcg gcc tat gtg ggc aat tgc gcg gtg ttc cag acc tcc 480																	
Leu	Ala	Pro	Ser	Ala	Tyr	Val	Gly	Asn	Cys	Ala	Val	Phe	Gln	Thr	Ser		
					150				155						160		
gac gcg ctg cgc cgc gtg cag cgc gtc gcc tac cgc acc cgc cag ctc 528																	
Asp	Ala	Leu	Arg	Arg	Val	Gln	Arg	Val	Ala	Tyr	Arg	Thr	Arg	Gln	Leu		
				165					170					175			
gcc gac gcc cat ccg gcc cgc ggc ttc ggc tcc ggc gac cgg gcg gtg 576																	
Ala	Asp	Ala	His	Pro	Ala	Arg	Gly	Phe	Gly	Ser	Gly	Asp	Arg	Ala	Val		
			180					185					190				
tgg gag aag tcc ccg gac tgg cag ccc atc cgc aag gcc atc gag gag 624																	
Trp	Glu	Lys	Ser	Pro	Asp	Trp	Gln	Pro	Ile	Arg	Lys	Ala	Ile	Glu	Glu		
		195					200					205					
ctg ctc gtc acc ttc gaa tgg gac aag gcg ctc gcc ggc acc aat ttc 672																	
Leu	Leu	Val	Thr	Phe	Glu	Trp	Asp	Lys	Ala	Leu	Ala	Gly	Thr	Asn	Phe		
		210				215					220						
gtg gtg aag ccg atc ctc gac gag ctg ttc ctc aac cac ctg gcg cgc 720																	
Val	Val	Lys	Pro	Ile	Leu	Asp	Glu	Leu	Phe	Leu	Asn	His	Leu	Ala	Arg		
					230					235					240		
ctg ctc cac gtg gag ggc gac gag ctc gac agc ctc gtg ctg cgg aac 768																	
Leu	Leu	His	Val	Glu	Gly	Asp	Glu	Leu	Asp	Ser	Leu	Val	Leu	Arg	Asn		
				245					250					255			
ctt cac ggc gac gcc cag cgc cac gcc cgc tgg acg gcc gcg ctc ggc 816																	
Leu	His	Gly	Asp	Ala	Gln	Arg	His	Ala	Arg	Trp	Thr	Ala	Ala	Leu	Gly		
			260					265					270				
cgc ttc gcc gtc gag cag aac gtg aac aac cgc acg gtc ctg cgc gac 864																	
Arg	Phe	Ala	Val	Glu	Gln	Asn	Val	Asn	Asn	Arg	Thr	Val	Leu	Arg	Asp		
			275				280					285					
gcc atc gcc ggc tgg cac gag acc ggc gag gcg gtc ctc gcc gcg ggc 912																	
Ala	Ile	Ala	Gly	Trp	His	Glu	Thr	Gly	Glu	Ala	Val	Leu	Ala	Ala	Gly		
		290				295					300						
gcc ggg atg ctt gcg agc cgc gcc ccc agc gcg gat gcg gcc aag atc 960																	
Ala	Gly	Met	Leu	Ala	Ser	Arg	Ala	Pro	Ser	Ala	Asp	Ala	Ala	Lys	Ile		
		305			310				315					320			
gcc gac gag gtc cgc gcc acg ctc gcg cag ctg cac gcc aat gcg ggc 1008																	
Ala	Asp	Glu	Val	Arg	Ala	Thr	Leu	Ala	Gln	Leu	His	Ala	Asn	Ala	Gly		
				325					330				335				
ctc ggg cac gat gcc tga 1026																	
Leu	Gly	His	Asp	Ala													
			340														
<210> 16																	
<211> 341																	
<212> PRT																	
<213> Xanthobacta sp.																	
<400> 16																	
Met	Thr	Gln	Gln	Arg	Pro	Thr	Arg	Thr	Arg	Glu	Arg	Lys	Lys	Thr	Trp		

1	5	10	15												
Thr	Ala	Phe	Gly	Asn	Leu	Gly	Arg	Lys	Pro	Thr	Asp	Tyr	Glu	Val	Val
			20					25					30		
Thr	His	Asn	Met	Asn	His	Thr	Met	Arg	Gly	Thr	Pro	Leu	Glu	Leu	Ser
		35					40					45			
Pro	Thr	Val	His	Ala	Asn	Val	Trp	Leu	Lys	Lys	Asn	Arg	Asp	Glu	Ile
	50					55					60				
Ala	Leu	Lys	Val	Asp	Ser	Trp	Asp	Leu	Phe	Arg	Asp	Pro	Asp	Arg	Thr
65					70					75					80
Thr	Tyr	Asp	Thr	Tyr	Val	Lys	Met	Gln	Asp	Asp	Gln	Glu	Thr	Tyr	Val
				85					90					95	
Asp	Asn	Leu	Leu	Leu	Ser	Tyr	Thr	Gly	Glu	Gly	Arg	Tyr	Asp	Glu	Glu
			100					105					110		
Leu	Ser	Ser	Arg	Ser	Leu	Asp	Leu	Leu	Ser	Ala	Gly	Leu	Thr	Pro	Thr
		115					120					125			
Arg	Tyr	Leu	Gly	His	Gly	Leu	Gln	Met	Leu	Ala	Ala	Tyr	Ile	Gln	Gln
	130					135					140				
Leu	Ala	Pro	Ser	Ala	Tyr	Val	Gly	Asn	Cys	Ala	Val	Phe	Gln	Thr	Ser
145					150					155					160
Asp	Ala	Leu	Arg	Arg	Val	Gln	Arg	Val	Ala	Tyr	Arg	Thr	Arg	Gln	Leu
				165					170					175	
Ala	Asp	Ala	His	Pro	Ala	Arg	Gly	Phe	Gly	Ser	Gly	Asp	Arg	Ala	Val
			180					185					190		
Trp	Glu	Lys	Ser	Pro	Asp	Trp	Gln	Pro	Ile	Arg	Lys	Ala	Ile	Glu	Glu
	195						200					205			
Leu	Leu	Val	Thr	Phe	Glu	Trp	Asp	Lys	Ala	Leu	Ala	Gly	Thr	Asn	Phe
	210					215					220				
Val	Val	Lys	Pro	Ile	Leu	Asp	Glu	Leu	Phe	Leu	Asn	His	Leu	Ala	Arg
225					230					235					240
Leu	Leu	His	Val	Glu	Gly	Asp	Glu	Leu	Asp	Ser	Leu	Val	Leu	Arg	Asn
				245					250					255	
Leu	His	Gly	Asp	Ala	Gln	Arg	His	Ala	Arg	Trp	Thr	Ala	Ala	Leu	Gly
			260					265					270		
Arg	Phe	Ala	Val	Glu	Gln	Asn	Val	Asn	Asn	Arg	Thr	Val	Leu	Arg	Asp
		275					280					285			
Ala	Ile	Ala	Gly	Trp	His	Glu	Thr	Gly	Glu	Ala	Val	Leu	Ala	Ala	Gly
	290					295					300				
Ala	Gly	Met	Leu	Ala	Ser	Arg	Ala	Pro	Ser	Ala	Asp	Ala	Ala	Lys	Ile
305					310					315					320
Ala	Asp	Glu	Val	Arg	Ala	Thr	Leu	Ala	Gln	Leu	His	Ala	Asn	Ala	Gly
				325					330					335	
Leu	Gly	His	Asp	Ala											
			340												

<210> 17
 <211> 267
 <212> DNA
 <213> Xanthobacta sp.

<220>
 <221> CDS
 <222> (1)..(267)

<400> 17
 atg tct ttg ttc ccc atc gtg ggc cgc ttc gtg ggg gat ttc gtc ccc 48
 Met Ser Leu Phe Pro Ile Val Gly Arg Phe Val Gly Asp Phe Val Pro
 1 5 10 15

cac ctg gtg gcg gtg gac acc tct gac acc atc gat cag atc gcc gag 96
 His Leu Val Ala Val Asp Thr Ser Asp Thr Ile Asp Gln Ile Ala Glu
 20 25 30

aag gtg gcg gtc cac acg gtc ggg cgg cgc ttg ccg ccc gat ccc acc 144
 Lys Val Ala Val His Thr Val Gly Arg Arg Leu Pro Pro Asp Pro Thr
 35 40 45

gcc acc ggc tat gag gtg ctc ctc gac ggc gag acc ctg gac ggg ggc 192
 Ala Thr Gly Tyr Glu Val Leu Leu Asp Gly Glu Thr Leu Asp Gly Gly
 50 55 60

gcc acc ctg gag gcc atc atg acc aag cgc gag atg ctg ccc ctg cag 240
 Ala Thr Leu Glu Ala Ile Met Thr Lys Arg Glu Met Leu Pro Leu Gln
 65 70 75 80

tgg ttc gac gtg agg ttc aag aag tga 267
 Trp Phe Asp Val Arg Phe Lys Lys
 85

<210> 18
 <211> 88
 <212> PRT
 <213> Xanthobacta sp.

<400> 18
 Met Ser Leu Phe Pro Ile Val Gly Arg Phe Val Gly Asp Phe Val Pro
 1 5 10 15

His Leu Val Ala Val Asp Thr Ser Asp Thr Ile Asp Gln Ile Ala Glu
 20 25 30

Lys Val Ala Val His Thr Val Gly Arg Arg Leu Pro Pro Asp Pro Thr
 35 40 45

Ala Thr Gly Tyr Glu Val Leu Leu Asp Gly Glu Thr Leu Asp Gly Gly
 50 55 60

Ala Thr Leu Glu Ala Ile Met Thr Lys Arg Glu Met Leu Pro Leu Gln
 65 70 75 80

Trp Phe Asp Val Arg Phe Lys Lys
 85

<210> 19
 <211> 1584
 <212> DNA
 <213> Methylococcus capsulatas

<220>
 <221> CDS
 <222> (1)..(1584)

<400> 19
 atg gca ctt agc acc gca acc aag gcc gcg acg gac gcg ctg gct gcc 48
 Met Ala Leu Ser Thr Ala Thr Lys Ala Ala Thr Asp Ala Leu Ala Ala
 1 5 10 15

aat cgg gca ccc acc agc gtg aat gca cag gaa gtg cac cgt tgg ctc 96
 Asn Arg Ala Pro Thr Ser Val Asn Ala Gln Glu Val His Arg Trp Leu
 20 25 30

cag agc ttc aac tgg gat ttc aag aac aac cgg acc aag tac gcc acc 144
 Gln Ser Phe Asn Trp Asp Phe Lys Asn Asn Arg Thr Lys Tyr Ala Thr
 35 40 45

aag tac aag atg gcg aac gag acc aag gaa cag ttc aag ctg atc gcc 192

36

Lys	Tyr	Lys	Met	Ala	Asn	Glu	Thr	Lys	Glu	Gln	Phe	Lys	Leu	Ile	Ala		
50						55					60						
aag	gaa	tat	gcg	cgc	atg	gag	gca	gtc	aag	gac	gaa	agg	cag	ttc	ggt	240	
Lys	Glu	Tyr	Ala	Arg	Met	Glu	Ala	Val	Lys	Asp	Glu	Arg	Gln	Phe	Gly		
65					70					75					80		
agc	ctg	cag	gat	gcg	ctg	acc	cgc	ctc	aac	gcc	ggt	gtt	cgc	gtt	cat	288	
Ser	Leu	Gln	Asp	Ala	Leu	Thr	Arg	Leu	Asn	Ala	Gly	Val	Arg	Val	His		
				85					90					95			
ccg	aag	tgg	aac	gag	acc	atg	aaa	gtg	gtt	tcg	aac	ttc	ctg	gaa	gtg	336	
Pro	Lys	Trp	Asn	Glu	Thr	Met	Lys	Val	Val	Ser	Asn	Phe	Leu	Glu	Val		
			100					105					110				
ggc	gaa	tac	aac	gcc	atc	gcc	gct	acc	ggg	atg	ctg	tgg	gat	tcc	gcc	384	
Gly	Glu	Tyr	Asn	Ala	Ile	Ala	Ala	Thr	Gly	Met	Leu	Trp	Asp	Ser	Ala		
		115				120						125					
cag	gcg	gcg	gaa	cag	aag	aac	ggc	tat	ctg	gcc	cag	gtg	ttg	gat	gaa	432	
Gln	Ala	Ala	Glu	Gln	Lys	Asn	Gly	Tyr	Leu	Ala	Gln	Val	Leu	Asp	Glu		
	130					135					140						
atc	cgc	cac	acc	cac	cag	tgt	gcc	tac	gtc	aac	tac	tac	ttc	gcg	aag	480	
Ile	Arg	His	Thr	His	Gln	Cys	Ala	Tyr	Val	Asn	Tyr	Tyr	Phe	Ala	Lys		
	145				150					155					160		
aac	ggc	cag	gac	ccg	gcc	ggt	cac	aac	gat	gct	cgc	cgc	acc	cgt	acc	528	
Asn	Gly	Gln	Asp	Pro	Ala	Gly	His	Asn	Asp	Ala	Arg	Arg	Thr	Arg	Thr		
				165					170					175			
atc	ggt	ccg	ctg	tgg	aag	ggc	atg	aag	cgc	gtg	ttt	tcc	gac	ggc	ttc	576	
Ile	Gly	Pro	Leu	Trp	Lys	Gly	Met	Lys	Arg	Val	Phe	Ser	Asp	Gly	Phe		
			180					185					190				
att	tcc	ggc	gac	gcc	gtg	gaa	tgc	tcc	ctc	aac	ctg	cag	ctg	gtg	ggt	624	
Ile	Ser	Gly	Asp	Ala	Val	Glu	Cys	Ser	Leu	Asn	Leu	Gln	Leu	Val	Gly		
		195				200						205					
gag	gcc	tgc	ttc	acc	aat	ccg	ctg	atc	gtc	gca	gtg	acc	gaa	tgg	gct	672	
Glu	Ala	Cys	Phe	Thr	Asn	Pro	Leu	Ile	Val	Ala	Val	Thr	Glu	Trp	Ala		
	210					215					220						
gcc	gcc	aac	ggc	gat	gaa	atc	acc	ccg	acg	gtg	ttc	ctg	tcg	atc	gag	720	
Ala	Ala	Asn	Gly	Asp	Glu	Ile	Thr	Pro	Thr	Val	Phe	Leu	Ser	Ile	Glu		
	225				230					235					240		
acc	gac	gaa	ctg	cgc	cac	atg	gcc	aac	ggt	tac	cag	acc	gtc	gtt	tcc	768	
Thr	Asp	Glu	Leu	Arg	His	Met	Ala	Asn	Gly	Tyr	Gln	Thr	Val	Val	Ser		
				245					250					255			
atc	gcc	aac	gat	ccg	gct	tcc	gcc	aag	tat	ctc	aac	acg	gac	ctg	aac	816	
Ile	Ala	Asn	Asp	Pro	Ala	Ser	Ala	Lys	Tyr	Leu	Asn	Thr	Asp	Leu	Asn		
			260					265					270				
aac	gcc	ttc	tgg	acc	cag	cag	aag	tac	ttc	acg	ccg	gtg	ttg	ggc	atg	864	
Asn	Ala	Phe	Trp	Thr	Gln	Gln	Lys	Tyr	Phe	Thr	Pro	Val	Leu	Gly	Met		
		275					280					285					
ctg	ttc	gag	tat	ggc	tcc	aag	ttc	aag	gtc	gag	ccg	tgg	gtc	aag	acg	912	
Leu	Phe	Glu	Tyr	Gly	Ser	Lys	Phe	Lys	Val	Glu	Pro	Trp	Val	Lys	Thr		
	290					295					300						
tgg	gac	cgc	tgg	gtg	tac	gag	gac	tgg	ggc	ggc	atc	tgg	atc	ggc	cgt	960	
Trp	Asp	Arg	Trp	Val	Tyr	Glu	Asp	Trp	Gly	Gly	Ile	Trp	Ile	Gly	Arg		
	305				310					315					320		
ctg	ggc	aag	tac	ggg	gtg	gag	tcg	ccg	cgc	agc	ctc	aag	gac	gcc	aag	1008	
Leu	Gly	Lys	Tyr	Gly	Val	Glu	Ser	Pro	Arg	Ser	Leu	Lys	Asp	Ala	Lys		
				325					330					335			
cag	gac	gct	tac	tgg	gct	cac	cac	gac	ctg	tat	ctg	ctg	gct	tat	gcg	1056	
Gln	Asp	Ala	Tyr	Trp	Ala	His	His	Asp	Leu	Tyr	Leu	Leu	Ala	Tyr	Ala		
			340					345					350				
ctg	tgg	ccg	acc	ggc	ttc	ttc	cgt	ctg	gcg	ctg	ccg	gat	cag	gaa	gaa	1104	

Leu Trp Pro Thr Gly Phe Phe Arg Leu Ala Leu Pro Asp Gln Glu Glu
 355 360 365
 atg gag tgg ttc gag gcc aac tac ccc ggc tgg tac gac cac tac ggc 1152
 Met Glu Trp Phe Glu Ala Asn Tyr Pro Gly Trp Tyr Asp His Tyr Gly
 370 375 380
 aag atc tac gag gaa tgg cgc gcc cgc ggt tgc gag gat ccg tcc tcg 1200
 Lys Ile Tyr Glu Glu Trp Arg Ala Arg Gly Cys Glu Asp Pro Ser Ser
 385 390 395 400
 ggc ttc atc ccg ctg atg tgg ttc atc gaa aac aac cat ccc atc tac 1248
 Gly Phe Ile Pro Leu Met Trp Phe Ile Glu Asn Asn His Pro Ile Tyr
 405 410 415
 atc gat cgc gtg tcg caa gtg ccg ttc tgc ccg agc ttg gcc aag ggc 1296
 Ile Asp Arg Val Ser Gln Val Pro Phe Cys Pro Ser Leu Ala Lys Gly
 420 425 430
 gcc agc acc ctg cgc gtg cac gag tac aac ggc gag atg cac acc ttc 1344
 Ala Ser Thr Leu Arg Val His Glu Tyr Asn Gly Glu Met His Thr Phe
 435 440 445
 agc gac cag tgg ggc gag cgc atg tgg ctg gcc gag ccg gag cgc tac 1392
 Ser Asp Gln Trp Gly Glu Arg Met Trp Leu Ala Glu Pro Glu Arg Tyr
 450 455 460
 gag tgc cag aac atc ttc gaa cag tac gaa gga cgc gaa ctg tcg gaa 1440
 Glu Cys Gln Asn Ile Phe Glu Gln Tyr Glu Gly Arg Glu Leu Ser Glu
 465 470 475 480
 gtg atc gcc gaa ctg cac ggg ctg cgc agt gat ggc aag acc ctg atc 1488
 Val Ile Ala Glu Leu His Gly Leu Arg Ser Asp Gly Lys Thr Leu Ile
 485 490 495
 gcc cag ccg cat gtc cgt ggc gac aag ctg tgg acg ttg gac gat atc 1536
 Ala Gln Pro His Val Arg Gly Asp Lys Leu Trp Thr Leu Asp Asp Ile
 500 505 510
 aaa cgc ctg aac tgc gtc ttc aag aac ccg gtg aag gca ttc aat tga 1584
 Lys Arg Leu Asn Cys Val Phe Lys Asn Pro Val Lys Ala Phe Asn
 515 520 525
 <210> 20
 <211> 527
 <212> PRT
 <213> Methylococcus capsulatas
 <400> 20
 Met Ala Leu Ser Thr Ala Thr Lys Ala Ala Thr Asp Ala Leu Ala Ala
 1 5 10 15
 Asn Arg Ala Pro Thr Ser Val Asn Ala Gln Glu Val His Arg Trp Leu
 20 25 30
 Gln Ser Phe Asn Trp Asp Phe Lys Asn Asn Arg Thr Lys Tyr Ala Thr
 35 40 45
 Lys Tyr Lys Met Ala Asn Glu Thr Lys Glu Gln Phe Lys Leu Ile Ala
 50 55 60
 Lys Glu Tyr Ala Arg Met Glu Ala Val Lys Asp Glu Arg Gln Phe Gly
 65 70 75 80
 Ser Leu Gln Asp Ala Leu Thr Arg Leu Asn Ala Gly Val Arg Val His
 85 90 95
 Pro Lys Trp Asn Glu Thr Met Lys Val Val Ser Asn Phe Leu Glu Val
 100 105 110
 Gly Glu Tyr Asn Ala Ile Ala Ala Thr Gly Met Leu Trp Asp Ser Ala
 115 120 125
 Gln Ala Ala Glu Gln Lys Asn Gly Tyr Leu Ala Gln Val Leu Asp Glu

38

130	135	140
Ile Arg His Thr His Gln Cys Ala Tyr Val Asn Tyr Tyr Phe Ala Lys 145 150 155 160		
Asn Gly Gln Asp Pro Ala Gly His Asn Asp Ala Arg Arg Thr Arg Thr 165 170 175		
Ile Gly Pro Leu Trp Lys Gly Met Lys Arg Val Phe Ser Asp Gly Phe 180 185 190		
Ile Ser Gly Asp Ala Val Glu Cys Ser Leu Asn Leu Gln Leu Val Gly 195 200 205		
Glu Ala Cys Phe Thr Asn Pro Leu Ile Val Ala Val Thr Glu Trp Ala 210 215 220		
Ala Ala Asn Gly Asp Glu Ile Thr Pro Thr Val Phe Leu Ser Ile Glu 225 230 235 240		
Thr Asp Glu Leu Arg His Met Ala Asn Gly Tyr Gln Thr Val Val Ser 245 250 255		
Ile Ala Asn Asp Pro Ala Ser Ala Lys Tyr Leu Asn Thr Asp Leu Asn 260 265 270		
Asn Ala Phe Trp Thr Gln Gln Lys Tyr Phe Thr Pro Val Leu Gly Met 275 280 285		
Leu Phe Glu Tyr Gly Ser Lys Phe Lys Val Glu Pro Trp Val Lys Thr 290 295 300		
Trp Asp Arg Trp Val Tyr Glu Asp Trp Gly Gly Ile Trp Ile Gly Arg 305 310 315 320		
Leu Gly Lys Tyr Gly Val Glu Ser Pro Arg Ser Leu Lys Asp Ala Lys 325 330 335		
Gln Asp Ala Tyr Trp Ala His His Asp Leu Tyr Leu Leu Ala Tyr Ala 340 345 350		
Leu Trp Pro Thr Gly Phe Phe Arg Leu Ala Leu Pro Asp Gln Glu Glu 355 360 365		
Met Glu Trp Phe Glu Ala Asn Tyr Pro Gly Trp Tyr Asp His Tyr Gly 370 375 380		
Lys Ile Tyr Glu Glu Trp Arg Ala Arg Gly Cys Glu Asp Pro Ser Ser 385 390 395 400		
Gly Phe Ile Pro Leu Met Trp Phe Ile Glu Asn Asn His Pro Ile Tyr 405 410 415		
Ile Asp Arg Val Ser Gln Val Pro Phe Cys Pro Ser Leu Ala Lys Gly 420 425 430		
Ala Ser Thr Leu Arg Val His Glu Tyr Asn Gly Glu Met His Thr Phe 435 440 445		
Ser Asp Gln Trp Gly Glu Arg Met Trp Leu Ala Glu Pro Glu Arg Tyr 450 455 460		
Glu Cys Gln Asn Ile Phe Glu Gln Tyr Glu Gly Arg Glu Leu Ser Glu 465 470 475 480		
Val Ile Ala Glu Leu His Gly Leu Arg Ser Asp Gly Lys Thr Leu Ile 485 490 495		
Ala Gln Pro His Val Arg Gly Asp Lys Leu Trp Thr Leu Asp Asp Ile 500 505 510		
Lys Arg Leu Asn Cys Val Phe Lys Asn Pro Val Lys Ala Phe Asn 515 520 525		

<210> 21

<211> 1170
 <212> DNA
 <213> Methylococcus capsulatas

<220>
 <221> CDS
 <222> (1) .. (1170)

<400> 21
 atg agc atg tta gga gaa aga cgc cgc ggt ctg acc gat ccg gaa atg 48
 Met Ser Met Leu Gly Glu Arg Arg Arg Gly Leu Thr Asp Pro Glu Met
 1 5 10 15

gcg gcc gtc att ttg aag gcg ctt cct gaa gct ccg ctg gac ggc aac 96
 Ala Ala Val Ile Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Asn
 20 25 30

aac aag atg ggt tat ttc gtc acc ccc cgc tgg aaa cgc ttg acg gaa 144
 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu
 35 40 45

tat gaa gcc ctg acc gtt tat gcg cag ccc aac gcc gac tgg atc gcc 192
 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala
 50 55 60

ggc ggc ctg gac tgg ggc gac tgg acc cag aaa ttc cac ggc ggc cgc 240
 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg
 65 70 75 80

cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 288
 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe
 85 90 95

aag cac cgt gac ccg ctc cgc cgt tgg cat gcg ccg tac gtc aag gac 336
 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp
 100 105 110

aag gcc gag gaa tgg cgc tac acc gac cgc ttc ctg cag ggt tac tcc 384
 Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser
 115 120 125

gcc gac ggt cag atc cgg gcg atg aac ccg acc tgg cgg gac gag ttc 432
 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe
 130 135 140

atc aac cgg tat tgg ggc gcc ttc ctg ttc aac gaa tac gga ttg ttc 480
 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe
 145 150 155 160

aac gct cat tcg cag ggc gcc cgg gag gcg ctg tcg gac gta acc cgc 528
 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg
 165 170 175

gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac atc gcc cag atg 576
 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met
 180 185 190

atc caa ctc gaa cgg ggt ttc ctc gcc aag atc gta ccc ggt ttc gac 624
 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp
 195 200 205

gag tcc aca gcg gtg ccg aag gcc gaa tgg acg aac ggg gag gtc tac 672
 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr
 210 215 220

aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 720
 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp
 225 230 235 240

tgg aac gag agc gct ttc tcg gtg cac gcc gtc tat gac gcg ctg ttc 768
 Trp Asn Glu Ser Ala Phe Ser Val His Ala Val Tyr Asp Ala Leu Phe
 245 250 255

ggt cag ttc gtc cgc cgc gag ttc ttt cag cgg ctg gct ccc cgc ttc 816
 Gly Gln Phe Val Arg Arg Glu Phe Phe Gln Arg Leu Ala Pro Arg Phe

260	265	270	
ggc gac aat ctg acg cca ttc ttc atc aac cag gcc cag aca tac ttc			864
Gly Asp Asn Leu Thr Pro Phe Phe Ile Asn Gln Ala Gln Thr Tyr Phe			
275	280	285	
cag atc gcc aag cag ggc gta cag gat ctg tat tac aac tgt ctg ggt			912
Gln Ile Ala Lys Gln Gly Val Gln Asp Leu Tyr Tyr Asn Cys Leu Gly			
290	295	300	
gac gat ccg gag ttc agc gat tac aac cgt acc gtg atg cgc aac tgg			960
Asp Asp Pro Glu Phe Ser Asp Tyr Asn Arg Thr Val Met Arg Asn Trp			
305	310	315	320
acc ggc aag tgg ctg gag ccc acg atc gcc gct ctg cgc gac ttc atg			1008
Thr Gly Lys Trp Leu Glu Pro Thr Ile Ala Ala Leu Arg Asp Phe Met			
	325	330	335
ggg ctg ttt gcg aag ctg ccg gcg ggc acc act gac aag gaa gaa atc			1056
Gly Leu Phe Ala Lys Leu Pro Ala Gly Thr Thr Asp Lys Glu Glu Ile			
	340	345	350
acc gcg tcc ctg tac cgg gtg gtc gac gac tgg atc gag gac tac gcc			1104
Thr Ala Ser Leu Tyr Arg Val Val Asp Asp Trp Ile Glu Asp Tyr Ala			
	355	360	365
agc gcg atc gac ttc aag gcg gac cgc gat cag atc gtt aaa gcg gtt			1152
Ser Ala Ile Asp Phe Lys Ala Asp Arg Asp Gln Ile Val Lys Ala Val			
	370	375	380
ctg gca gga ttg aaa taa			1170
Leu Ala Gly Leu Lys			
385			
<210>	22		
<211>	389		
<212>	PRT		
<213>	Methylococcus capsulatas		
<400>	22		
Met Ser Met Leu Gly Glu Arg Arg Arg Gly Leu Thr Asp Pro Glu Met			
1	5	10	15
Ala Ala Val Ile Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Asn			
	20	25	30
Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu			
	35	40	45
Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala			
	50	55	60
Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg			
65	70	75	80
Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe			
	85	90	95
Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp			
	100	105	110
Lys Ala Glu Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser			
	115	120	125
Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe			
	130	135	140
Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe			
145	150	155	160
Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg			
	165	170	175
Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met			

180 185 190
 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp
 195 200 205
 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr
 210 215 220
 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp
 225 230 235 240
 Trp Asn Glu Ser Ala Phe Ser Val His Ala Val Tyr Asp Ala Leu Phe
 245 250 255
 Gly Gln Phe Val Arg Arg Glu Phe Phe Gln Arg Leu Ala Pro Arg Phe
 260 265 270
 Gly Asp Asn Leu Thr Pro Phe Phe Ile Asn Gln Ala Gln Thr Tyr Phe
 275 280 285
 Gln Ile Ala Lys Gln Gly Val Gln Asp Leu Tyr Tyr Asn Cys Leu Gly
 290 295 300
 Asp Asp Pro Glu Phe Ser Asp Tyr Asn Arg Thr Val Met Arg Asn Trp
 305 310 315 320
 Thr Gly Lys Trp Leu Glu Pro Thr Ile Ala Ala Leu Arg Asp Phe Met
 325 330 335
 Gly Leu Phe Ala Lys Leu Pro Ala Gly Thr Thr Asp Lys Glu Glu Ile
 340 345 350
 Thr Ala Ser Leu Tyr Arg Val Val Asp Asp Trp Ile Glu Asp Tyr Ala
 355 360 365
 Ser Ala Ile Asp Phe Lys Ala Asp Arg Asp Gln Ile Val Lys Ala Val
 370 375 380
 Leu Ala Gly Leu Lys
 385

<210> 23
 <211> 513
 <212> DNA
 <213> Methylococcus capsulatas

<220>
 <221> CDS
 <222> (1)..(513)

<400> 23
 atg gcg aaa ctg ggt ata cac agc aac gac acc cgc gac gcc tgg gtg 48
 Met Ala Lys Leu Gly Ile His Ser Asn Asp Thr Arg Asp Ala Trp Val
 1 5 10 15
 aac aag atc gcg cag ctc aac acc ctg gaa aaa gcg gcc gag atg ctg 96
 Asn Lys Ile Ala Gln Leu Asn Thr Leu Glu Lys Ala Ala Glu Met Leu
 20 25 30
 aag cag ttc cgg atg gac cac acc acg ccg ttc cgc aac agc tac gaa 144
 Lys Gln Phe Arg Met Asp His Thr Thr Pro Phe Arg Asn Ser Tyr Glu
 35 40 45
 ctg gac aac gac tac ctc tgg atc gag gcc aag ctc gaa gag aag gtc 192
 Leu Asp Asn Asp Tyr Leu Trp Ile Glu Ala Lys Leu Glu Glu Lys Val
 50 55 60
 gcc gtc ctc aag gca cgc gcc ttc aac gag gtg gac ttc cgt cat aag 240
 Ala Val Leu Lys Ala Arg Ala Phe Asn Glu Val Asp Phe Arg His Lys
 65 70 75 80
 acc gct ttc ggc gag gat gcc aag tcc gtt ctg gac ggc acc gtc gcg 288
 Thr Ala Phe Gly Glu Asp Ala Lys Ser Val Leu Asp Gly Thr Val Ala
 85 90 95

aag atg aac gcg gcc aag gac aag tgg gag gcg gag aag atc cat atc 336
 Lys Met Asn Ala Ala Lys Asp Lys Trp Glu Ala Glu Lys Ile His Ile
 100 105 110
 ggt ttc cgc cag gcc tac aag ccg ccg atc atg ccg gtg aac tat ttc 384
 Gly Phe Arg Gln Ala Tyr Lys Pro Pro Ile Met Pro Val Asn Tyr Phe
 115 120 125
 ctg gac ggc gag cgt cag ttg ggg acc ccg ctg atg gaa ctg cgc aac 432
 Leu Asp Gly Glu Arg Gln Leu Gly Thr Arg Leu Met Glu Leu Arg Asn
 130 135 140
 ctc aac tac tac gac acg ccg ctg gaa gaa ctg cgc aaa cag cgc ggt 480
 Leu Asn Tyr Tyr Asp Thr Pro Leu Glu Glu Leu Arg Lys Gln Arg Gly
 145 150 155 160
 gtg cgg gtg gtg cat ctg cag tcg ccg cac tga 513
 Val Arg Val Val His Leu Gln Ser Pro His
 165 170

<210> 24
 <211> 170
 <212> PRT
 <213> *Methylococcus capsulatus*

<400> 24

Met Ala Lys Leu Gly Ile His Ser Asn Asp Thr Arg Asp Ala Trp Val
 1 5 10 15
 Asn Lys Ile Ala Gln Leu Asn Thr Leu Glu Lys Ala Ala Glu Met Leu
 20 25 30
 Lys Gln Phe Arg Met Asp His Thr Thr Pro Phe Arg Asn Ser Tyr Glu
 35 40 45
 Leu Asp Asn Asp Tyr Leu Trp Ile Glu Ala Lys Leu Glu Glu Lys Val
 50 55 60
 Ala Val Leu Lys Ala Arg Ala Phe Asn Glu Val Asp Phe Arg His Lys
 65 70 75 80
 Thr Ala Phe Gly Glu Asp Ala Lys Ser Val Leu Asp Gly Thr Val Ala
 85 90 95
 Lys Met Asn Ala Ala Lys Asp Lys Trp Glu Ala Glu Lys Ile His Ile
 100 105 110
 Gly Phe Arg Gln Ala Tyr Lys Pro Pro Ile Met Pro Val Asn Tyr Phe
 115 120 125
 Leu Asp Gly Glu Arg Gln Leu Gly Thr Arg Leu Met Glu Leu Arg Asn
 130 135 140
 Leu Asn Tyr Tyr Asp Thr Pro Leu Glu Glu Leu Arg Lys Gln Arg Gly
 145 150 155 160
 Val Arg Val Val His Leu Gln Ser Pro His
 165 170

<210> 25
 <211> 1206
 <212> DNA
 <213> *Pseudomonas oleovorans*

<220>
 <221> CDS
 <222> (1)..(1206)

<400> 25
 atg ctt gag aaa cac aga gtt ctg gat tcc gct cca gag tac gta gat 48
 Met Leu Glu Lys His Arg Val Leu Asp Ser Ala Pro Glu Tyr Val Asp

1	5	10	15	
aaa aag aaa tat ctc tgg ata cta tca act ttg tgg ccg gct act ccg				96
Lys Lys Lys Tyr Leu Trp Ile Leu Ser Thr Leu Trp Pro Ala Thr Pro				
20	25	30		
atg atc gga atc tgg ctt gca aat gaa act ggt tgg ggg att ttt tat				144
Met Ile Gly Ile Trp Leu Ala Asn Glu Thr Gly Trp Gly Ile Phe Tyr				
35	40	45		
ggg ctg gta ttg ctc gta tgg tac ggc gca ctt cca ttg ctt gat gcg				192
Gly Leu Val Leu Leu Val Trp Tyr Gly Ala Leu Pro Leu Leu Asp Ala				
50	55	60		
atg ttt ggt gag gac ttt aat aat ccg cct gaa gaa gtg gtg ccg aaa				240
Met Phe Gly Glu Asp Phe Asn Asn Pro Pro Glu Glu Val Val Pro Lys				
65	70	75	80	
cta gag aag gag cgg tac tat cga gtt ttg aca tat cta aca gtt cct				288
Leu Glu Lys Glu Arg Tyr Tyr Arg Val Leu Thr Tyr Leu Thr Val Pro				
85	90	95		
atg cat tac gct gca tta att gtg tca gca tgg tgg gtc gga act cag				336
Met His Tyr Ala Ala Leu Ile Val Ser Ala Trp Trp Val Gly Thr Gln				
100	105	110		
cca atg tct tgg ctt gaa att ggt gcg ctt gcc ttg tca ctg ggt atc				384
Pro Met Ser Trp Leu Glu Ile Gly Ala Leu Ala Leu Ser Leu Gly Ile				
115	120	125		
gtg aac gga cta gcg ctc aat aca gga cac gaa ctc ggt cac aag aag				432
Val Asn Gly Leu Ala Leu Asn Thr Gly His Glu Leu Gly His Lys Lys				
130	135	140		
gag act ttt gat cgt tgg atg gcc aaa att gtg ttg gct gtc gta ggg				480
Glu Thr Phe Asp Arg Trp Met Ala Lys Ile Val Leu Ala Val Val Gly				
145	150	155	160	
tac ggt cac ttc ttt att gag cat aat aag ggt cat cac cgt gat gtc				528
Tyr Gly His Phe Phe Ile Glu His Asn Lys Gly His His Arg Asp Val				
165	170	175		
gct aca ccg atg gat cct gca aca tcc cgg atg gga gaa agc att tat				576
Ala Thr Pro Met Asp Pro Ala Thr Ser Arg Met Gly Glu Ser Ile Tyr				
180	185	190		
aag ttt tca atc cgt gag atc cca gga gca ttt att cgt gct tgg ggg				624
Lys Phe Ser Ile Arg Glu Ile Pro Gly Ala Phe Ile Arg Ala Trp Gly				
195	200	205		
ctt gag gaa caa cgc ctt tcg cgc cgt ggc caa agc gtt tgg agt ttc				672
Leu Glu Glu Gln Arg Leu Ser Arg Arg Gly Gln Ser Val Trp Ser Phe				
210	215	220		
gat aat gaa atc ctc caa cca atg atc atc aca gtt att ctt tac gcc				720
Asp Asn Glu Ile Leu Gln Pro Met Ile Ile Thr Val Ile Leu Tyr Ala				
225	230	235	240	
gtt ctc ctt gcc ttg ttt gga cct aag atg ctg gtg ttc ctg ccg att				768
Val Leu Leu Ala Leu Phe Gly Pro Lys Met Leu Val Phe Leu Pro Ile				
245	250	255		
caa atg gct ttc ggt tgg tgg cag ctg acc agt gcg aac tat att gaa				816
Gln Met Ala Phe Gly Trp Trp Gln Leu Thr Ser Ala Asn Tyr Ile Glu				
260	265	270		
cat tac ggc ttg ctc cgt caa aaa atg gag gac ggt cga tat gag cat				864
His Tyr Gly Leu Leu Arg Gln Lys Met Glu Asp Gly Arg Tyr Glu His				
275	280	285		
caa aag ccg cac cat tct tgg aat agt aat cac atc gtc tct aat cta				912
Gln Lys Pro His His Ser Trp Asn Ser Asn His Ile Val Ser Asn Leu				
290	295	300		
gtg ctg ttc cac ctt cag cgg cac tcg gat cac cac gcg cat cca aca				960
Val Leu Phe His Leu Gln Arg His Ser Asp His His Ala His Pro Thr				

305	310	315	320	
cgt tct tat cag tca ctt cgg gat ttt ccc ggc ctg ccg gct ctt ccg				1008
Arg Ser Tyr Gln Ser Leu Arg Asp Phe Pro Gly Leu Pro Ala Leu Pro	325	330	335	
acg ggt tac cct ggt gca ttt ttg atg gcg atg att cct cag tgg ttt				1056
Thr Gly Tyr Pro Gly Ala Phe Leu Met Ala Met Ile Pro Gln Trp Phe	340	345	350	
aga tca gtt atg gat ccc aag gta gta gat tgg gct ggt ggt gac ctt				1104
Arg Ser Val Met Asp Pro Lys Val Val Asp Trp Ala Gly Gly Asp Leu	355	360	365	
aat aag atc caa att gat gat tcg atg cga gaa acc tat ttg aaa aaa				1152
Asn Lys Ile Gln Ile Asp Asp Ser Met Arg Glu Thr Tyr Leu Lys Lys	370	375	380	
ttt ggc act agt agt gct ggt cat agt tcg agt acc tct gcg gta gca				1200
Phe Gly Thr Ser Ser Ala Gly His Ser Ser Ser Thr Ser Ala Val Ala	385	390	400	
tcg tag				1206
Ser				
<210>	26			
<211>	401			
<212>	PRT			
<213>	Pseudomonas oleovorans			
<400>	26			
Met Leu Glu Lys His Arg Val Leu Asp Ser Ala Pro Glu Tyr Val Asp				
1	5	10	15	
Lys Lys Lys Tyr Leu Trp Ile Leu Ser Thr Leu Trp Pro Ala Thr Pro				
	20	25	30	
Met Ile Gly Ile Trp Leu Ala Asn Glu Thr Gly Trp Gly Ile Phe Tyr				
	35	40	45	
Gly Leu Val Leu Leu Val Trp Tyr Gly Ala Leu Pro Leu Leu Asp Ala				
	50	55	60	
Met Phe Gly Glu Asp Phe Asn Asn Pro Pro Glu Glu Val Val Pro Lys				
65	70	75	80	
Leu Glu Lys Glu Arg Tyr Tyr Arg Val Leu Thr Tyr Leu Thr Val Pro				
	85	90	95	
Met His Tyr Ala Ala Leu Ile Val Ser Ala Trp Trp Val Gly Thr Gln				
	100	105	110	
Pro Met Ser Trp Leu Glu Ile Gly Ala Leu Ala Leu Ser Leu Gly Ile				
	115	120	125	
Val Asn Gly Leu Ala Leu Asn Thr Gly His Glu Leu Gly His Lys Lys				
	130	135	140	
Glu Thr Phe Asp Arg Trp Met Ala Lys Ile Val Leu Ala Val Val Gly				
145	150	155	160	
Tyr Gly His Phe Phe Ile Glu His Asn Lys Gly His His Arg Asp Val				
	165	170	175	
Ala Thr Pro Met Asp Pro Ala Thr Ser Arg Met Gly Glu Ser Ile Tyr				
	180	185	190	
Lys Phe Ser Ile Arg Glu Ile Pro Gly Ala Phe Ile Arg Ala Trp Gly				
	195	200	205	
Leu Glu Glu Gln Arg Leu Ser Arg Arg Gly Gln Ser Val Trp Ser Phe				
	210	215	220	

45

Asp Asn Glu Ile Leu Gln Pro Met Ile Ile Thr Val Ile Leu Tyr Ala
 225 230 235 240
 Val Leu Leu Ala Leu Phe Gly Pro Lys Met Leu Val Phe Leu Pro Ile
 245 250 255
 Gln Met Ala Phe Gly Trp Trp Gln Leu Thr Ser Ala Asn Tyr Ile Glu
 260 265 270
 His Tyr Gly Leu Leu Arg Gln Lys Met Glu Asp Gly Arg Tyr Glu His
 275 280 285
 Gln Lys Pro His His Ser Trp Asn Ser Asn His Ile Val Ser Asn Leu
 290 295 300
 Val Leu Phe His Leu Gln Arg His Ser Asp His His Ala His Pro Thr
 305 310 315 320
 Arg Ser Tyr Gln Ser Leu Arg Asp Phe Pro Gly Leu Pro Ala Leu Pro
 325 330 335
 Thr Gly Tyr Pro Gly Ala Phe Leu Met Ala Met Ile Pro Gln Trp Phe
 340 345 350
 Arg Ser Val Met Asp Pro Lys Val Val Asp Trp Ala Gly Gly Asp Leu
 355 360 365
 Asn Lys Ile Gln Ile Asp Asp Ser Met Arg Glu Thr Tyr Leu Lys Lys
 370 375 380
 Phe Gly Thr Ser Ser Ala Gly His Ser Ser Ser Thr Ser Ala Val Ala
 385 390 395 400
 Ser

<210> 27
 <211> 1560
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (1)..(1560)

<400> 27
 atg gac act tct gtg cag aag aag aaa ctc ggt tta aag aat cgc tac 48
 Met Asp Thr Ser Val Gln Lys Lys Lys Leu Gly Leu Lys Asn Arg Tyr
 1 5 10 15
 gca gcg atg acc cgc ggt ctt ggc tgg cag acc agc tac cag ccg atg 96
 Ala Ala Met Thr Arg Gly Leu Gly Trp Gln Thr Ser Tyr Gln Pro Met
 20 25 30
 gag aaa gtg ttt ccg tac gac aag tac gaa ggc atc aag atc cac gat 144
 Glu Lys Val Phe Pro Tyr Asp Lys Tyr Glu Gly Ile Lys Ile His Asp
 35 40 45
 tgg gat aaa tgg gaa gac ccc ttc cgc ctg acc atg gac gcc tac tgg 192
 Trp Asp Lys Trp Glu Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
 50 55 60
 aaa tat cag ggc gag aag gaa aaa aag ctt tac gcc gtc atc gac gct 240
 Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
 65 70 75 80
 ttc gcg cag aac aac ggg cag ttg agc att tcc gac gcg cga tat gtc 288
 Phe Ala Gln Asn Asn Gly Gln Leu Ser Ile Ser Asp Ala Arg Tyr Val
 85 90 95
 aac gca ctc aag gtg ttt atc cag ggt gtg aca ccg ttg gag tat atg 336
 Asn Ala Leu Lys Val Phe Ile Gln Gly Val Thr Pro Leu Glu Tyr Met
 100 105 110

gca cac cga ggt ttt gcc cac att ggt cgg cat ttt acg ggt gaa ggg Ala His Arg Gly Phe Ala His Ile Gly Arg His Phe Thr Gly Glu Gly 115 120 125	384
gca cgt gtt gct tgc cag atg cag tcc atc gac gag ctg cgt cac ttc Ala Arg Val Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Phe 130 135 140	432
cag acc gaa atg cat gct ctc tcg cac tac aac aag tat ttt aac ggt Gln Thr Glu Met His Ala Leu Ser His Tyr Asn Lys Tyr Phe Asn Gly 145 150 155 160	480
ctg cac aac tcc atc cat tgg tac gac cgg gtt tgg tat ttg tcg gtg Leu His Asn Ser Ile His Trp Tyr Asp Arg Val Trp Tyr Leu Ser Val 165 170 175	528
ccc aag tca ttt ttt gaa gac gcg gcc acc ggt gga ccg ttc gag ttt Pro Lys Ser Phe Phe Glu Asp Ala Ala Thr Gly Gly Pro Phe Glu Phe 180 185 190	576
ctt acc gcg gtg agc ttt tcg ttc gaa tat gtg ttg acc aac ctg ctg Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu 195 200 205	624
ttt gtc ccc ttc atg tcg ggt gct gct tac aac ggg gac atg tct acg Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr 210 215 220	672
gtc act ttc ggt ttt tcg gcg caa agt gac gaa tcg cgc cac atg aca Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr 225 230 235 240	720
ctc ggc atc gaa tgc atc aag ttc atg cta gaa cag gat ccg gac aac Leu Gly Ile Glu Cys Ile Lys Phe Met Leu Glu Gln Asp Pro Asp Asn 245 250 255	768
gtg ccc atc gtg cag cgc tgg atc gac aag tgg ttc tgg cgc ggc tat Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr 260 265 270	816
cgg ctg ttg agc atc gtg gcc atg atg cag gac tac atg ctg ccc aac Arg Leu Leu Ser Ile Val Ala Met Met Gln Asp Tyr Met Leu Pro Asn 275 280 285	864
cgg gtg atg agc tgg cgc gag agc tgg gag atg tac gtc gag cag aac Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Val Glu Gln Asn 290 295 300	912
ggc ggc gcg ctg ttc aag gat ctt gcg cgt tat ggc atc cgc aag ccc Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Lys Pro 305 310 315 320	960
aag ggc tgg gac cag gct tgc gaa ggc aag gac cac atc agc cat cag Lys Gly Trp Asp Gln Ala Cys Glu Gly Lys Asp His Ile Ser His Gln 325 330 335	1008
acc ttc gcc gta ttc tat aac tat aac gcc gcg gcc ccc atc cac acc Thr Phe Ala Val Phe Tyr Asn Tyr Asn Ala Ala Ala Pro Ile His Thr 340 345 350	1056
tgg gtt ccc aca aaa gaa gaa atg gga tgg ctg tcg gag aag tac ccc Trp Val Pro Thr Lys Glu Glu Met Gly Trp Leu Ser Glu Lys Tyr Pro 355 360 365	1104
gag acg ttc gac aag tat tac cgt ccg cgt tgg gac tac tgg cgc gag Glu Thr Phe Asp Lys Tyr Tyr Arg Pro Arg Trp Asp Tyr Trp Arg Glu 370 375 380	1152
cag gcc gcc aag ggc aac cgt ttc tac aac aag acg ctg ccg atg ctc Gln Ala Ala Lys Gly Asn Arg Phe Tyr Asn Lys Thr Leu Pro Met Leu 385 390 395 400	1200
tgc act acc tgc cag att ccg atg ata ttc acc gag cct ggc gac gca Cys Thr Thr Cys Gln Ile Pro Met Ile Phe Thr Glu Pro Gly Asp Ala 405 410 415	1248

acc aag atc tgc tat cgc gag tcg gcc tac ctc ggc gac aag tat cac 1296
 Thr Lys Ile Cys Tyr Arg Glu Ser Ala Tyr Leu Gly Asp Lys Tyr His
 420 425 430

ttc tgc agc gac cac tgc aag gag att ttt gac aac gaa ccc gaa aag 1344
 Phe Cys Ser Asp His Cys Lys Glu Ile Phe Asp Asn Glu Pro Glu Lys
 435 440 445

ttc gtg cag tca tgg ctt ccg ccg cag caa gtg tat caa gga aac tgt 1392
 Phe Val Gln Ser Trp Leu Pro Pro Gln Gln Val Tyr Gln Gly Asn Cys
 450 455 460

ttc aag ccg gat gcc gat ccg acc aag gag ggt ttt gat ccc ttg atg 1440
 Phe Lys Pro Asp Ala Asp Pro Thr Lys Glu Gly Phe Asp Pro Leu Met
 465 470 475 480

gcc ttg ctc gac tac tac aac ctg aat gta ggc cgg gac aac ttc gat 1488
 Ala Leu Leu Asp Tyr Tyr Asn Leu Asn Val Gly Arg Asp Asn Phe Asp
 485 490 495

ttc gag gga tcg gaa gac caa aag aac ttt gct gcc tgg cgt gga gag 1536
 Phe Glu Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Glu
 500 505 510

gtc ttg caa gga gaa gcc aaa tga 1560
 Val Leu Gln Gly Glu Ala Lys
 515

<210> 28
 <211> 519
 <212> PRT
 <213> Burkholderia cepacia

<400> 28

Met Asp Thr Ser Val Gln Lys Lys Lys Leu Gly Leu Lys Asn Arg Tyr
 1 5 10 15

Ala Ala Met Thr Arg Gly Leu Gly Trp Gln Thr Ser Tyr Gln Pro Met
 20 25 30

Glu Lys Val Phe Pro Tyr Asp Lys Tyr Glu Gly Ile Lys Ile His Asp
 35 40 45

Trp Asp Lys Trp Glu Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
 50 55 60

Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
 65 70 75 80

Phe Ala Gln Asn Asn Gly Gln Leu Ser Ile Ser Asp Ala Arg Tyr Val
 85 90 95

Asn Ala Leu Lys Val Phe Ile Gln Gly Val Thr Pro Leu Glu Tyr Met
 100 105 110

Ala His Arg Gly Phe Ala His Ile Gly Arg His Phe Thr Gly Glu Gly
 115 120 125

Ala Arg Val Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Phe
 130 135 140

Gln Thr Glu Met His Ala Leu Ser His Tyr Asn Lys Tyr Phe Asn Gly
 145 150 155 160

Leu His Asn Ser Ile His Trp Tyr Asp Arg Val Trp Tyr Leu Ser Val
 165 170 175

Pro Lys Ser Phe Phe Glu Asp Ala Ala Thr Gly Gly Pro Phe Glu Phe
 180 185 190

Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
 195 200 205

48

Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
 210 215 220
 Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
 225 230 235 240
 Leu Gly Ile Glu Cys Ile Lys Phe Met Leu Glu Gln Asp Pro Asp Asn
 245 250 255
 Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
 260 265 270
 Arg Leu Leu Ser Ile Val Ala Met Met Gln Asp Tyr Met Leu Pro Asn
 275 280 285
 Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Val Glu Gln Asn
 290 295 300
 Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Lys Pro
 305 310 315 320
 Lys Gly Trp Asp Gln Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
 325 330 335
 Thr Phe Ala Val Phe Tyr Asn Tyr Asn Ala Ala Ala Pro Ile His Thr
 340 345 350
 Trp Val Pro Thr Lys Glu Glu Met Gly Trp Leu Ser Glu Lys Tyr Pro
 355 360 365
 Glu Thr Phe Asp Lys Tyr Tyr Arg Pro Arg Trp Asp Tyr Trp Arg Glu
 370 375 380
 Gln Ala Ala Lys Gly Asn Arg Phe Tyr Asn Lys Thr Leu Pro Met Leu
 385 390 395 400
 Cys Thr Thr Cys Gln Ile Pro Met Ile Phe Thr Glu Pro Gly Asp Ala
 405 410 415
 Thr Lys Ile Cys Tyr Arg Glu Ser Ala Tyr Leu Gly Asp Lys Tyr His
 420 425 430
 Phe Cys Ser Asp His Cys Lys Glu Ile Phe Asp Asn Glu Pro Glu Lys
 435 440 445
 Phe Val Gln Ser Trp Leu Pro Pro Gln Gln Val Tyr Gln Gly Asn Cys
 450 455 460
 Phe Lys Pro Asp Ala Asp Pro Thr Lys Glu Gly Phe Asp Pro Leu Met
 465 470 475 480
 Ala Leu Leu Asp Tyr Tyr Asn Leu Asn Val Gly Arg Asp Asn Phe Asp
 485 490 495
 Phe Glu Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Glu
 500 505 510
 Val Leu Gln Gly Glu Ala Lys
 515

<210> 29
 <211> 996
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (1)..(996)

<400> 29
 atg acc atc gat ttg aag acg cgg gaa atc aaa cca ctg cgt cac acc
 Met Thr Ile Asp Leu Lys Thr Arg Glu Ile Lys Pro Leu Arg His Thr
 1 5 10 15

tac acg cac gtg gct caa tac atc ggg gcc gat aaa gcc gct tcg cgc Tyr Thr His Val Ala Gln Tyr Ile Gly Ala Asp Lys Ala Ala Ser Arg 20 25 30	96
tat cag gaa ggc act gta ggt gct caa ccc gca gcg aat ttt cat tac Tyr Gln Glu Gly Thr Val Gly Ala Gln Pro Ala Ala Asn Phe His Tyr 35 40 45	144
cgg ccc acg tgg gat ccc gag cat gaa ctg ttc gac acg tcg cgt acc Arg Pro Thr Trp Asp Pro Glu His Glu Leu Phe Asp Thr Ser Arg Thr 50 55 60	192
gcg att caa atg aag gac tgg tat gcg ctg aaa gac ccg cgt cag ttc Ala Ile Gln Met Lys Asp Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe 65 70 75 80	240
tac tac gcg tcg tgg acg atg acc cga gcg cgg cag caa gac gcg atg Tyr Tyr Ala Ser Trp Thr Met Thr Arg Ala Arg Gln Gln Asp Ala Met 85 90 95	288
gaa tcc aac ttc gag ttt gtc gag tcg cgc ggc atg atc gat ctc gtt Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Gly Met Ile Asp Leu Val 100 105 110	336
tcc gat gag gtt cga caa cgg gcg ctt tcc gtt ctc gtg cct ttg cgt Ser Asp Glu Val Arg Gln Arg Ala Leu Ser Val Leu Val Pro Leu Arg 115 120 125	384
cac gcg gcc tgg ggc gcg aac atg aac aac tcc cag atc tgt gcc cta His Ala Ala Trp Gly Ala Asn Met Asn Asn Ser Gln Ile Cys Ala Leu 130 135 140	432
ggt tat ggc acg acc ttc act gcg ccg gct atg ttc cac gca atg gac Gly Tyr Gly Thr Thr Phe Thr Ala Pro Ala Met Phe His Ala Met Asp 145 150 155 160	480
aat ctg ggt gta gcg cag tat ctc aca cga ctg gcg ctg gta atg tct Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Val Met Ser 165 170 175	528
gga ccc gat ctt ctt gac gaa gcc aag caa gcc tgg atg acg agt ccc Gly Pro Asp Leu Leu Asp Glu Ala Lys Gln Ala Trp Met Thr Ser Pro 180 185 190	576
gat tgg caa ccg ttg cgt cgt tat gtg gaa aac act ctg gtg ctg caa Asp Trp Gln Pro Leu Arg Arg Tyr Val Glu Asn Thr Leu Val Leu Gln 195 200 205	624
gat ccg gtg gaa ctg ttc atc gcc caa aat ctg gcg ctc gac ggt ctt Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu 210 215 220	672
ctt tat ccc atg atc tac ggc gct ttc gtc gac gat tac atc gca ctc Leu Tyr Pro Met Ile Tyr Gly Ala Phe Val Asp Asp Tyr Ile Ala Leu 225 230 235 240	720
aac ggt ggt agc gca gtg gca atg cta acc act ttc atg ccc gag tgg Asn Gly Gly Ser Ala Val Ala Met Leu Thr Thr Phe Met Pro Glu Trp 245 250 255	768
cat gac gaa tcc agt cgc tgg gtc gat gcg gta gta aag acc atg gcg His Asp Glu Ser Ser Arg Trp Val Asp Ala Val Val Lys Thr Met Ala 260 265 270	816
acg gaa tcg gag gat aac aaa gcg ctg ctc att cac tgg ttg cgt acc Thr Glu Ser Glu Asp Asn Lys Ala Leu Leu Ile His Trp Leu Arg Thr 275 280 285	864
tgg gaa gat cag gcg gcg tca gcg ttg ttg cct gtc gct gaa atg gct Trp Glu Asp Gln Ala Ala Ser Ala Leu Leu Pro Val Ala Glu Met Ala 290 295 300	912
ttg gcg gaa aac ggc cac gac gcc ttg gaa gaa gta agg cag caa ctt Leu Ala Glu Asn Gly His Asp Ala Leu Glu Glu Val Arg Gln Gln Leu 305 310 315 320	960

50

cgt gcc cgc gtt gcg aag gcc ggg att gtt ctg taa
 Arg Ala Arg Val Ala Lys Ala Gly Ile Val Leu
 325 330

996

<210> 30
 <211> 331
 <212> PRT
 <213> Burkholderia cepacia

<400> 30

Met Thr Ile Asp Leu Lys Thr Arg Glu Ile Lys Pro Leu Arg His Thr
 1 5 10 15
 Tyr Thr His Val Ala Gln Tyr Ile Gly Ala Asp Lys Ala Ala Ser Arg
 20 25 30
 Tyr Gln Glu Gly Thr Val Gly Ala Gln Pro Ala Ala Asn Phe His Tyr
 35 40 45
 Arg Pro Thr Trp Asp Pro Glu His Glu Leu Phe Asp Thr Ser Arg Thr
 50 55 60
 Ala Ile Gln Met Lys Asp Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe
 65 70 75 80
 Tyr Tyr Ala Ser Trp Thr Met Thr Arg Ala Arg Gln Gln Asp Ala Met
 85 90 95
 Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Gly Met Ile Asp Leu Val
 100 105 110
 Ser Asp Glu Val Arg Gln Arg Ala Leu Ser Val Leu Val Pro Leu Arg
 115 120 125
 His Ala Ala Trp Gly Ala Asn Met Asn Asn Ser Gln Ile Cys Ala Leu
 130 135 140
 Gly Tyr Gly Thr Thr Phe Thr Ala Pro Ala Met Phe His Ala Met Asp
 145 150 155 160
 Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Val Met Ser
 165 170 175
 Gly Pro Asp Leu Leu Asp Glu Ala Lys Gln Ala Trp Met Thr Ser Pro
 180 185 190
 Asp Trp Gln Pro Leu Arg Arg Tyr Val Glu Asn Thr Leu Val Leu Gln
 195 200 205
 Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu
 210 215 220
 Leu Tyr Pro Met Ile Tyr Gly Ala Phe Val Asp Asp Tyr Ile Ala Leu
 225 230 235 240
 Asn Gly Gly Ser Ala Val Ala Met Leu Thr Thr Phe Met Pro Glu Trp
 245 250 255
 His Asp Glu Ser Ser Arg Trp Val Asp Ala Val Val Lys Thr Met Ala
 260 265 270
 Thr Glu Ser Glu Asp Asn Lys Ala Leu Leu Ile His Trp Leu Arg Thr
 275 280 285
 Trp Glu Asp Gln Ala Ala Ser Ala Leu Leu Pro Val Ala Glu Met Ala
 290 295 300
 Leu Ala Glu Asn Gly His Asp Ala Leu Glu Glu Val Arg Gln Gln Leu
 305 310 315 320
 Arg Ala Arg Val Ala Lys Ala Gly Ile Val Leu
 325 330

<210> 31
 <211> 357
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (1)..(357)

<400> 31
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 Met Ser Val Val Ala Leu Lys Pro Tyr Lys Phe Pro Ala Arg Asp Ala
 1 5 10 15
 cgc gaa aac ttt ccg gcg ccg ttg ctg ttt atc ggc tgg gaa gac cat 96
 Arg Glu Asn Phe Pro Ala Pro Leu Leu Phe Ile Gly Trp Glu Asp His
 20 25 30
 ctg ttg ttt gcg gca cct gtt gcc ttg ccc ctg ccg tcg gac acg ttg 144
 Leu Leu Phe Ala Ala Pro Val Ala Leu Pro Leu Pro Ser Asp Thr Leu
 35 40 45
 ttc ggt gcg ctg tgc acc cag gtg ttg ccc ggc act tat ggc tat cac 192
 Phe Gly Ala Leu Cys Thr Gln Val Leu Pro Gly Thr Tyr Gly Tyr His
 50 55 60
 ccc gat ttc tca aag atc gac tgg agc cag gtg cag tgg ttt aag tcc 240
 Pro Asp Phe Ser Lys Ile Asp Trp Ser Gln Val Gln Trp Phe Lys Ser
 65 70 75 80
 ggc cag ccg tgg cat ccc gac ccg gcg aag tcg ctg gct gaa aac ggt 288
 Gly Gln Pro Trp His Pro Asp Pro Ala Lys Ser Leu Ala Glu Asn Gly
 85 90 95
 ctg acg cac aaa gac gtg atc cgc ttt cgc acg cct ggc ttg aac ggt 336
 Leu Thr His Lys Asp Val Ile Arg Phe Arg Thr Pro Gly Leu Asn Gly
 100 105 110
 ctg agc ggt tcc tgc aat tga 357
 Leu Ser Gly Ser Cys Asn
 115

<210> 32
 <211> 118
 <212> PRT
 <213> Burkholderia cepacia

<400> 32
 Met Ser Val Val Ala Leu Lys Pro Tyr Lys Phe Pro Ala Arg Asp Ala
 1 5 10 15
 Arg Glu Asn Phe Pro Ala Pro Leu Leu Phe Ile Gly Trp Glu Asp His
 20 25 30
 Leu Leu Phe Ala Ala Pro Val Ala Leu Pro Leu Pro Ser Asp Thr Leu
 35 40 45
 Phe Gly Ala Leu Cys Thr Gln Val Leu Pro Gly Thr Tyr Gly Tyr His
 50 55 60
 Pro Asp Phe Ser Lys Ile Asp Trp Ser Gln Val Gln Trp Phe Lys Ser
 65 70 75 80
 Gly Gln Pro Trp His Pro Asp Pro Ala Lys Ser Leu Ala Glu Asn Gly
 85 90 95
 Leu Thr His Lys Asp Val Ile Arg Phe Arg Thr Pro Gly Leu Asn Gly
 100 105 110
 Leu Ser Gly Ser Cys Asn
 115

<210> 33
 <211> 1143
 <212> DNA
 <213> *Bacillus stearothermophilus*

<220>
 <221> CDS
 <222> (1) .. (1143)

<400> 33
 atg gaa aaa aat aaa atg tta ata gaa gaa aag ttg gac act gct gct 48
 Met Glu Lys Asn Lys Met Leu Ile Glu Glu Lys Leu Asp Thr Ala Ala
 1 5 10 15
 ctt ctt gct aag gcg gag gaa ata ggc cgg att gct gag gaa gag gcg 96
 Leu Leu Ala Lys Ala Glu Glu Ile Gly Arg Ile Ala Glu Glu Glu Ala
 20 25 30
 ggt gaa gcg gac cgc aat gcc tgt ttc tcc gac cgg gtg gct agg gcc 144
 Gly Glu Ala Asp Arg Asn Ala Cys Phe Ser Asp Arg Val Ala Arg Ala
 35 40 45
 att aaa gaa gct gga ttc cac aag ctc atg cgt ccc aag cag tac gga 192
 Ile Lys Glu Ala Gly Phe His Lys Leu Met Arg Pro Lys Gln Tyr Gly
 50 55 60
 gga ctg caa gta gac ttg cga act tac ggg gag att gtc cgc aca gtg 240
 Gly Leu Gln Val Asp Leu Arg Thr Tyr Gly Glu Ile Val Arg Thr Val
 65 70 75 80
 gcc cgg tac agt gtt gcc gca gga tgg ctg acc tat ttt tat tcc atg 288
 Ala Arg Tyr Ser Val Ala Ala Gly Trp Leu Thr Tyr Phe Tyr Ser Met
 85 90 95
 cat gag gtt tgg gct gca tat ctg cct cca aaa ggc aga gaa gaa att 336
 His Glu Val Trp Ala Ala Tyr Leu Pro Pro Lys Gly Arg Glu Glu Ile
 100 105 110
 ttt gga caa gga ggg ctg ttg gca gac gtc gtt gcc cct gtt ggc cgg 384
 Phe Gly Gln Gly Gly Leu Leu Ala Asp Val Val Ala Pro Val Gly Arg
 115 120 125
 gtg gag aag gac ggg gac ggc tac cgt ctc tat ggg cag tgg aac ttc 432
 Val Glu Lys Asp Gly Asp Gly Tyr Arg Leu Tyr Gly Gln Trp Asn Phe
 130 135 140
 tgt agc ggt gtc ctc cat agt gac tgg atc gga ctt ggc gcc atg atg 480
 Cys Ser Gly Val Leu His Ser Asp Trp Ile Gly Leu Gly Ala Met Met
 145 150 155 160
 gag ctg cct gac ggc aat agt cct gag tac tgt ttg tta gtg ctg cct 528
 Glu Leu Pro Asp Gly Asn Ser Pro Glu Tyr Cys Leu Leu Val Leu Pro
 165 170 175
 aag tcg gat gtc cag atc gta gaa aat tgg gat acc atg ggc ctc cgc 576
 Lys Ser Asp Val Gln Ile Val Glu Asn Trp Asp Thr Met Gly Leu Arg
 180 185 190
 gct tcg gga agc aac ggg gta tta gtt gaa ggt gct tat gtt cca tta 624
 Ala Ser Gly Ser Asn Gly Val Leu Val Glu Gly Ala Tyr Val Pro Leu
 195 200 205
 cac cgg atc ttt ccg gct ggc cgg gtg atg gct cat ccg ctt ttc ttg 672
 His Arg Ile Phe Pro Ala Gly Arg Val Met Ala His Pro Leu Phe Leu
 210 215 220
 ctt ggg ttc cct tta gta tct tta ggc ggc gac gaa cga ttg gtg tca 720
 Leu Gly Phe Pro Leu Val Ser Leu Gly Gly Asp Glu Arg Leu Val Ser
 225 230 235 240
 ctt ttc caa gaa cgc act gag aag cgc att cgt gtc ttc aaa ggc ggc 768
 Leu Phe Gln Glu Arg Thr Glu Lys Arg Ile Arg Val Phe Lys Gly Gly
 245 250 255
 gcg aaa gaa aag gat tct gcc gct agc cag cgg ctg tta gcc gag atg 816

Ala Lys Glu Lys Asp Ser Ala Ala Ser Gln Arg Leu Leu Ala Glu Met
 260 265 270

aaa aca gaa tta aat gca atg gaa ggc att gtg gaa caa tat atc cgc 864
 Lys Thr Glu Leu Asn Ala Met Glu Gly Ile Val Glu Gln Tyr Ile Arg
 275 280 285

cag ctt gag gct tgc caa aaa gaa gga aag acg gtg atg aac gat atg 912
 Gln Leu Glu Ala Cys Gln Lys Glu Gly Lys Thr Val Met Asn Asp Met
 290 295 300

gag cga gag cag cta ttc gca tgg cgt gga tat gtg gca aaa gcg tcc 960
 Glu Arg Glu Gln Leu Phe Ala Trp Arg Gly Tyr Val Ala Lys Ala Ser
 305 310 315 320

gcc aat att gcc gtc aga aca ctg tta act ctt gga ggc aat tcg atc 1008
 Ala Asn Ile Ala Val Arg Thr Leu Leu Thr Leu Gly Gly Asn Ser Ile
 325 330 335

ttt aaa ggc gat ccg gta gaa ctg ttc aca aga gat ttg cta gcg gtg 1056
 Phe Lys Gly Asp Pro Val Glu Leu Phe Thr Arg Asp Leu Leu Ala Val
 340 345 350

gcc gca cat cct aac tcc ctg tgg gag gat gcg atg gct gca tat gga 1104
 Ala Ala His Pro Asn Ser Leu Trp Glu Asp Ala Met Ala Ala Tyr Gly
 355 360 365

aga acg ata ttc ggg ctg cca ggg gac cca gtc tgg taa 1143
 Arg Thr Ile Phe Gly Leu Pro Gly Asp Pro Val Trp
 370 375 380

<210> 34
 <211> 380
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 34

Met Glu Lys Asn Lys Met Leu Ile Glu Glu Lys Leu Asp Thr Ala Ala
 1 5 10 15

Leu Leu Ala Lys Ala Glu Glu Ile Gly Arg Ile Ala Glu Glu Glu Ala
 20 25 30

Gly Glu Ala Asp Arg Asn Ala Cys Phe Ser Asp Arg Val Ala Arg Ala
 35 40 45

Ile Lys Glu Ala Gly Phe His Lys Leu Met Arg Pro Lys Gln Tyr Gly
 50 55 60

Gly Leu Gln Val Asp Leu Arg Thr Tyr Gly Glu Ile Val Arg Thr Val
 65 70 75 80

Ala Arg Tyr Ser Val Ala Ala Gly Trp Leu Thr Tyr Phe Tyr Ser Met
 85 90 95

His Glu Val Trp Ala Ala Tyr Leu Pro Pro Lys Gly Arg Glu Glu Ile
 100 105 110

Phe Gly Gln Gly Gly Leu Leu Ala Asp Val Val Ala Pro Val Gly Arg
 115 120 125

Val Glu Lys Asp Gly Asp Gly Tyr Arg Leu Tyr Gly Gln Trp Asn Phe
 130 135 140

Cys Ser Gly Val Leu His Ser Asp Trp Ile Gly Leu Gly Ala Met Met
 145 150 155 160

Glu Leu Pro Asp Gly Asn Ser Pro Glu Tyr Cys Leu Leu Val Leu Pro
 165 170 175

Lys Ser Asp Val Gln Ile Val Glu Asn Trp Asp Thr Met Gly Leu Arg
 180 185 190

Ala Ser Gly Ser Asn Gly Val Leu Val Glu Gly Ala Tyr Val Pro Leu

195	200	205	
His Arg Ile Phe Pro Ala Gly Arg Val Met Ala His Pro Leu Phe Leu			
210	215	220	
Leu Gly Phe Pro Leu Val Ser Leu Gly Gly Asp Glu Arg Leu Val Ser			
225	230	235	240
Leu Phe Gln Glu Arg Thr Glu Lys Arg Ile Arg Val Phe Lys Gly Gly			
	245	250	255
Ala Lys Glu Lys Asp Ser Ala Ala Ser Gln Arg Leu Leu Ala Glu Met			
	260	265	270
Lys Thr Glu Leu Asn Ala Met Glu Gly Ile Val Glu Gln Tyr Ile Arg			
	275	280	285
Gln Leu Glu Ala Cys Gln Lys Glu Gly Lys Thr Val Met Asn Asp Met			
	290	295	300
Glu Arg Glu Gln Leu Phe Ala Trp Arg Gly Tyr Val Ala Lys Ala Ser			
305	310	315	320
Ala Asn Ile Ala Val Arg Thr Leu Leu Thr Leu Gly Gly Asn Ser Ile			
	325	330	335
Phe Lys Gly Asp Pro Val Glu Leu Phe Thr Arg Asp Leu Leu Ala Val			
	340	345	350
Ala Ala His Pro Asn Ser Leu Trp Glu Asp Ala Met Ala Ala Tyr Gly			
	355	360	365
Arg Thr Ile Phe Gly Leu Pro Gly Asp Pro Val Trp			
	370	375	380

<210> 35
 <211> 1191
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> CDS
 <222> (1)..(1191)

<400> 35	
atg gcg att cgc atc aat acg gcg acg ttt caa tca gac ctg tac cgt	48
Met Ala Ile Arg Ile Asn Thr Ala Thr Phe Gln Ser Asp Leu Tyr Arg	
1 5 10 15	
tca ttc gcg ttt cct caa ccg aaa cct ctc aga tct ccc aaa ttc gcc	96
Ser Phe Ala Phe Pro Gln Pro Lys Pro Leu Arg Ser Pro Lys Phe Ala	
20 25 30	
atg gct tcc acc att gga tcc gct aca acg aag gtt gaa agc acc aaa	144
Met Ala Ser Thr Ile Gly Ser Ala Thr Thr Lys Val Glu Ser Thr Lys	
35 40 45	
aag ccc ttt acc cct cca agg gag gtt cac caa cag gtg cta cac tca	192
Lys Pro Phe Thr Pro Pro Arg Glu Val His Gln Gln Val Leu His Ser	
50 55 60	
atg ccg cca caa aag atc gaa atc ttc aaa tcc atg gag ggt tgg gcc	240
Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Met Glu Gly Trp Ala	
65 70 75 80	
gaa aat aac ata ttg gtt cac cta aag cct gtc gaa aaa tgc tgg caa	288
Glu Asn Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln	
85 90 95	
gca cag gat ttc cta cca gat ccc gca tct gac gga ttt atg gaa caa	336
Ala Gln Asp Phe Leu Pro Asp Pro Ala Ser Asp Gly Phe Met Glu Gln	
100 105 110	
gtg gag gaa tta cgg gct cgg gct aag gag att ccg gat gat tac ttt	384

Val	Glu	Glu	Leu	Arg	Ala	Arg	Ala	Lys	Glu	Ile	Pro	Asp	Asp	Tyr	Phe		
	115						120					125					
gtt gtt ttg gtt gga gat atg att act gaa gaa gca ctg cct act tac 432																	
Val	Val	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr		
	130					135					140						
caa aca atg ctt aat act ctt gat ggt gtg cgt gat gag acc ggg gct 480																	
Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala		
	145				150					155					160		
acc cta ctt ctt ggg cta gtc tgg act cgg gct tgg acc gct gaa gaa 528																	
Thr	Leu	Leu	Leu	Gly	Leu	Val	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu		
				165					170					175			
aac agg cac ggt gat ctt cta cat cag tat ctg tat ctt agt ggg cgg 576																	
Asn	Arg	His	Gly	Asp	Leu	Leu	His	Gln	Tyr	Leu	Tyr	Leu	Ser	Gly	Arg		
			180					185					190				
gtc gac atg agg cag att cag aag aca att cag tac ctc att ggg tct 624																	
Val	Asp	Met	Arg	Gln	Ile	Gln	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser		
		195					200					205					
gga atg gac ccc cgg acc gaa aac agt cct tac ctt ggg ttc atc tac 672																	
Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Ser	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr		
	210					215					220						
act tca ttt caa gag cgt gcc acc ttc atc tct cac gga aac aca gcc 720																	
Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala		
	225					230				235					240		
cgg cac gca aag gag cat ggt gac gtg aag ctg gct caa atg tgc ggt 768																	
Arg	His	Ala	Lys	Glu	His	Gly	Asp	Val	Lys	Leu	Ala	Gln	Met	Cys	Gly		
				245					250					255			
ata att gca gct gat gaa aaa agg cac gaa acc gcc tac aca aaa ata 816																	
Ile	Ile	Ala	Ala	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile		
			260					265					270				
gta gaa aaa ctc ttc gaa att gac ccg gac ggc act gtt ctc gct ttt 864																	
Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Leu	Ala	Phe		
		275					280					285					
gcc gac atg atg agg aaa aag atc tcc atg cct gca cac ttg atg tac 912																	
Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	Ala	His	Leu	Met	Tyr		
	290					295					300						
gat ggg cgt gat gat aac ctc ttc gaa aat ttc tca gct gtt gcc caa 960																	
Asp	Gly	Arg	Asp	Asp	Asn	Leu	Phe	Glu	Asn	Phe	Ser	Ala	Val	Ala	Gln		
	305				310				315						320		
agg ctc ggt gtg tac act gcg aag gac tat gca gac att ctg gag ttt 1008																	
Arg	Leu	Gly	Val	Tyr	Thr	Ala	Lys	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe		
				325				330					335				
ctg gtg ggc cgg tgg aag gtg gcg gat tta acc ggg ctt tct ggt gaa 1056																	
Leu	Val	Gly	Arg	Trp	Lys	Val	Ala	Asp	Leu	Thr	Gly	Leu	Ser	Gly	Glu		
			340					345					350				
ggg cgt aaa gcc caa gac tat gtg tgc ggg ctg gcc cca aga atc aga 1104																	
Gly	Arg	Lys	Ala	Gln	Asp	Tyr	Val	Cys	Gly	Leu	Ala	Pro	Arg	Ile	Arg		
		355				360						365					
agg ctt gag gag agg aac tcg gca agg gcg aag gaa agt gtg aac gtt 1152																	
Arg	Leu	Glu	Glu	Arg	Asn	Ser	Ala	Arg	Ala	Lys	Glu	Ser	Val	Asn	Val		
	370				375						380						
ccg ttc agc tgg atc ttt gat aga gaa gtg aag ctc tga 1191																	
Pro	Phe	Ser	Trp	Ile	Phe	Asp	Arg	Glu	Val	Lys	Leu						
	385				390					395							

<210> 36
 <211> 396
 <212> PRT
 <213> Helianthus annuus

<400> 36

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Met Ala Ile Arg Ile Asn Thr Ala Thr Phe Gln Ser Asp Leu Tyr Arg
1           5           10           15

Ser Phe Ala Phe Pro Gln Pro Lys Pro Leu Arg Ser Pro Lys Phe Ala
20           25           30

Met Ala Ser Thr Ile Gly Ser Ala Thr Thr Lys Val Glu Ser Thr Lys
35           40           45

Lys Pro Phe Thr Pro Pro Arg Glu Val His Gln Gln Val Leu His Ser
50           55           60

Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Met Glu Gly Trp Ala
65           70           75           80

Glu Asn Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln
85           90           95

Ala Gln Asp Phe Leu Pro Asp Pro Ala Ser Asp Gly Phe Met Glu Gln
100          105          110

Val Glu Glu Leu Arg Ala Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
115          120          125

Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
130          135          140

Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
145          150          155          160

Thr Leu Leu Leu Gly Leu Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
165          170          175

Asn Arg His Gly Asp Leu Leu His Gln Tyr Leu Tyr Leu Ser Gly Arg
180          185          190

Val Asp Met Arg Gln Ile Gln Lys Thr Ile Gln Tyr Leu Ile Gly Ser
195          200          205

Gly Met Asp Pro Arg Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr
210          215          220

Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
225          230          235          240

Arg His Ala Lys Glu His Gly Asp Val Lys Leu Ala Gln Met Cys Gly
245          250          255

Ile Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
260          265          270

Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Leu Ala Phe
275          280          285

Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Tyr
290          295          300

Asp Gly Arg Asp Asp Asn Leu Phe Glu Asn Phe Ser Ala Val Ala Gln
305          310          315          320

Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe
325          330          335

Leu Val Gly Arg Trp Lys Val Ala Asp Leu Thr Gly Leu Ser Gly Glu
340          345          350

Gly Arg Lys Ala Gln Asp Tyr Val Cys Gly Leu Ala Pro Arg Ile Arg
355          360          365

Arg Leu Glu Glu Arg Asn Ser Ala Arg Ala Lys Glu Ser Val Asn Val
370          375          380

Pro Phe Ser Trp Ile Phe Asp Arg Glu Val Lys Leu
385          390          395

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